

FIGURE 1A

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1  TGGAAGGGTT AATTTACTCC AAGAAAAGGC AAGAAATCCT TGATTTGTGG GTCTATCACA
61  CACAAGGCTT CTTCCCTGAT TGGCAAAACT ACACACCGGG GCCAGGGGTC AGATATCCAC
121 TGACCTTTGG ATGGTGCTAC AAGCTAGTGC CAGTTGACCC AGGGGAGGTG GAAGAGGCCA
181 ACGGAGGAGA AGACAACTGT TTGCTACACC CTATGAGCCA ACATGGAGCA GAGGATGAAG
241 ATAGAGAAGT ATTAAAGTGG AAGTTTGACA GCCTCCTAGC ACGCAGACAC ATGGCCCGCG
301 AGCTACATCC GGAGTATTAC AAAGACTGCT GACACAGAAG GGACTTTCCG CCTGGGACTT
361 TCCACTGGGG CGTTCCGGGA GGTGTGGTCT GGGCGGGACT TGGGAGTGGT CAACCCTCAG
421 ATGCTGCATA TAAGCAGCTG CTTTTCGCCT GTACTGGGTC TCTCTCGGTA GACCAGATCT
481 GAGCCTGGGA GCCCTCTGGC TATCTAGGGA ACCCACTGCT TAAGCCTCAA TAAAGCTTGC
541 CTTGAGTGCT TTAAGTAGTG TGTGCCATC TGTTGTGTGA CTCTGGTAAC TAGAGATCCC
601 TCAGACCCCT TGTGGTAGTG TGGAAAATCT CTAGCAGTGG CGCCGAACA GGGACCAGAA
661 AGTGAAAGTG AGACCAGAGG AGATCTCTCG ACGCAGGACT CGGCTTGCTG AAGTGCACAC
721 GGCAAGAGGC GAGAGGGGCG GCTGGTGAGT ACGCCAATTT TACTTGACTA GCGGAGGCTA
781 GAAGGAGAGA GATGGGTGCG AGAGCGTCAA TATTAAGCGG CGGAAAATTA GATAAATGGG
841 AAAGAATTAG GTTAAGGCCA GGGGGAAAAG AACATTATAT GTTAAAACAT CTAGTATGGG
901 CAAGCAGGGA GCTGGAAAGA TTTGCACTTA ACCCTGGCCT GTTAGAAACA TCAGAAGGCT
961 GTAAACAAAT AATAAACAG CTACAACCAG CTCCTCAGAC AGGAACAGAG GAACTTAGAT
1021 CATTATTCAA CACAGTAGCA ACTCTCTAAT GTGTACATAA AGGGATAGAG GTACGAGACA
1081 CCAAGGAAGC CTTAGACAAG ATGACGAAG AACAAAACAA ATGTCAGCAA AAAGCACAAC
1141 AGGCAAAAGC AGCTGACGAA AAGGTCAGTC AAAATTATCC TATAGTACAG AATGCCCAAG
1201 GGCAATGGT ACACCAAGCT ATATCACCTA GAACATTGAA TGCATGGATA AAAGTAATAG
1261 AGGAAAAGGC TTTCAATCCA GAGGAAATAC CCATGTTTAC AGCATTATCA GAAGGAGCCA
1321 CCCCACAAGA TTTAAACACA ATGTTAAATA CAGTGGGGGG ACATCAAGCA GCCATGCAAA
1381 TGTTAAAGA TACCATCAAT GAGGAGGCTG CAGAATGGGA TAGGACACAT CCAGTACATG
1441 CAGGGCCTGT TGCAACAGGC CAGATGAGAG AACCAAGGGG AAGTGACATA GCAGGAACTA
1501 CTAGTACCCT TCAGGAACAA ATAGCATGGA TGACAAGTAA TCCACCTATT CCAGTAGAAG
1561 ACATCTATAA AAGATGGATA ATTCTGGGGT TAAATAAAAT AGTAAGAATG TATAGCCCTG
1621 TTAGCATTTT GGACATAAAA CAAGGGCCAA AAGAACCCTT TAGAGACTAT GTAGACCGGT
1681 TCCTTTAAAC CTTAAGAGCT GAACAAGCTA CACAAGATGT AAAGAATTGG ATGACAGACA
1741 CCTTGTGGT CCAAATGCG AACCCAGATT GTAAGACCAT TTTAAGAGCA TTAGGACCAG
1801 GGGCCTCATT AGAAGAAATG ATGACAGCAT GTCAGGGAGT GGGAGGACCT AGCCATAAAG
1861 CAAGAGTGTT GGCTGAGGCA ATGAGCCAAG CAACACAGTAA CATACTAGTG CAGAGAAGCA
1921 ATTTTAAAGG CTCTAACAGA ATTATTAAAT GTTTCAACTG TGGCAAAGTA GGGCACATAG
1981 CCAGAAATTG CAGGGCCCTT AGGAAAAGG GCTGTTGGAA ATGTGGACAG GAAGGACACC
2041 AAATGAAAGA CTGTACTGAG AGGCAGGCTA ATTTTTTAGG GAAAATTGTT CTTCCCACA
2101 AGGGGAGGCC AGGGAATTTT CTCCAGAACA GACCAGAGCC AACAGCCCCA CCAGCAGAAC
2161 CAACAGCCCC ACCAGCAGAG AGCTTCAGGT TCGAGGAGAC AACCCCCGTG CCGAGGAAGG
2221 AGAAAGAGAG GGAACCTTTA ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTTGCTCT
2281 AATAAAAGTA GAGGGCCAGA TAAAGGAGGC TCTCTTAGAC ACAGGAGCAG ATGATACAGT
2341 ATTAGAAGAA ATAGATTTGC CAGGGAAATG GAAACCAAAA ATGATAGGGG GAATTGGAGG
2401 TTTTATCAAA GTAAACACAG ATGATCAAAAT ACTTATAGAA ATTTGTGGAA AAAAGGCTAT
2461 AGGTACAGTA TTAGTAGGGC CTACACCAGT CAACATAAAT GGAAGAAATC TGTTAACTCA
2521 GCTTGGATGC AACTAAATTT TTCCAATTAG TCCTATTGAA ACTGTACCAG TAAATTTAAA
2581 ACCAGGAATG GATGGCCCAA AGGTCAAACA ATGGCCATTG ACAGAAGAAA AAATAAAAGC
2641 ATTAACAGCA ATTTGTGAGG AAA TGAGAA GGAAGGAAA ATTACAAAA TTGGGCCTGA
2701 TAATCCATAT AACACTCCAG TATTTGCCAT AAAAAAGAAG GACAGTACTA AGTGGAGAAA
2761 ATTAGTAGAT TTCAGGGAAC TCAATAAAAG AACTCAAGAC TTTTGGGAAG TTCAATTAGG
2821 AATACCACAC CCAGCAGGAT TAAAAAGAA AAAATCAGTG ACAGTGCTAG ATGTGGGGGA
2881 TGCATATTTT TCAGTTCCTT TAGATGAAAG CTTTAGGAAA TATACTGCAT TCACCATACC
2941 TAGTATAAAC AATGAAACAC CAGGGATTAG ATATCAATAT AATGTGCTGC CACAGGGATG
3001 GAAAGGATCA CCAGCAATAT TCCAGAGTAG CATGACAAAA ATCTTAGAGC CTTTCAGAGC
3061 AAAAAATCCA GACATAGTTA TCTATCAATA TATGGATGAC TTGTATGTAG GATCTGACTT
3121 AGAAATAGGG CAACATAGAG CAAAAATAGA AGAGTTAAGG GAACATTTAT TGAAATGGGG

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FIGURE 1B

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3181 ATTTACAACA CCAGACAAGA AACATCAAAA AGAACCCCCA TTTCTTTGGA TGGGGTATGA
3241 ACTCCATCCT GACAAATGGA CAGTACAACC TATACTGCTG CCAGAAAAGG ATAGTTGGAC
3301 TGTCAATGAT ATACAGAAGT TAGTGGGAAA ATTAACTGG GCAAGTCAGA TTTACCCAGG
3361 GATTAAAGTA AGGCAACTCT GTAAACTCCT CAGGGGGGCC AAAGCACTAA CAGACATAGT
3421 ACCACTAACT GAAGAAGCAG AATTAGAATT GGCAGAGAAC AGGGAAATTT TAAGAGAACC
3481 AGTACATGGA GTATATTATG ATCCATCAAA AGACTTGATA GCTGAAATAC AGAAACAGGG
3541 GCATGAACAA TGGACATATC AAATTTATCA AGAACCATTT AAAAATCTGA AAACAGGGAA
3601 GTATGCAAAA ATGAGGACTA CCCACACTAA TGATGTAAAA CAGTTAACAG AGGCAGTGCA
3661 AAAAATAGCC ATGGAAAGCA TAGTAATATG GGGAAAGACT CCTAAATTTA GACTACCCAT
3721 CCAAAAAGAA ACATGGGAGA CATGGTGGAC AGACTATTGG CAAGCCACCT GGATCCCTGA
3781 GTGGGAGTTT GTTAATACCC CTCCCCTAGT AAAATTATGG TACCAACTAG AAAAAGATCC
3841 CATAGCAGGA GTAGAACTT TCTATGTAGA TGGAGCAACT AATAGGGAAG CTAAAATAGG
3901 AAAAGCAGGG TATGTTACTG ACAGAGGAAG GCAGAAAATT GTTACTCTAA CTAACACAAC
3961 AAATCAGAAG ACTGAGTTAC AAGCAATTCA GCTAGCTCTG CAGGATTCAG GATCAGAAGT
4021 AAACATAGTA ACAGACTCAC AGTATGCATT AGGAATCATT CAAGCACAAC CAGATAAGAG
4081 TGA CTCAGAG ATATTTAACC AAATAATAGA ACAGTTAATA AACAAGGAAA GAATCTACCT
4141 GTCATGGGTA CCAGCACATA AAGGAATTGG GGGAAATGAA CAAGTAGATA AATTAGTAAG
4201 TAAGGGAATT AGGAAAGTGT TGTTCCTAGA TGGAATAGAT AAAGCTCAAG AAGAGCATGA
4261 AAGGTACCAC AGCAATTGGA GAGCAATGGC TAATGAGTTT AATCTGCCAC CCATAGTAGC
4321 AAAAGAAATA GTAGCTAGCT GTGATAAATG TCAGCTAAAA GGGGAAGCCA TACATGGACA
4381 AGTCGACTGT AGTCCAGGGA TATGGCAATT AGATTGTACC CATTTAGAGG GAAAAATCAT
4441 CCTGGTAGCA GTCCATGTAG CTAGTGGCTA CATGGAAGCA GAGGTTATCC CAGCAGAAAC
4501 AGGACAAGAA ACAGCATATT TTATATTAAA ATTAGCAGGA AGATGGCCAG TCAAAGTAAT
4561 ACATACAGAC AATGGCAGTA ATTTTACCAG TACTGCAGTT AAGGCAGCCT GTTGGTGGGC
4621 AGGTATCCAA CAGGAATTTG GAATTCCTTA CAATCCCCAA AGTCAGGGAG TGGTAGAATC
4681 CATGAATAAA GAATTAAAGA AAATAATAGG ACAAGTAAGA GATCAAGCTG AGCACCTTAA
4741 GACAGCAGTA CAAATGGCAG TATTCATTCA CAATTTTAAA AGAAAAGGGG GAATTGGGGG
4801 GTACAGTGCA GGGGAAAGAA TAATAGACAT AATAGCAACA GACATACAAA CTAAAGAATT
4861 ACAAAAACAA ATTATAAGAA TTCAAATTT TCGGGTTTAT TACAGAGACA GCAGAGACCC
4921 TATTTGGAAG GGACCAGCCG AACTACTCTG GAAAGGTGAA GGGGTAGTAG TAATAGAAGA
4981 TAAAGGTGAC ATAAAGGTAG TACCAAGGAG GAAAGCAAAA ATCATTAGAG ATTATGGAAG
5041 ACAGATGGCA GGTGCTGATT GTGTGGCAGG TGGACAGGAT GAAGATTAGA GCATGGAATA
5101 GTTTAGTAAA GCACCATATG TATATATCAA GGAGAGCTAG TGGATGGGTC TACAGACATC
5161 ATTTTGAAAG CAGACATCCA AAAGTAAGTT CAGAAGTACA TATCCCATTA GGGGATGCTA
5221 GATTAGTAAT AAAAACATAT TGGGGTTTGC AGCAGGAGA AAGAGATTGG CATTTGGGTC
5281 ATGGAGTCTC CATAGAATGG AGACTGAGAG AATACAGCAC ACAAGTAGAC CCTGACCTGG
5341 CAGACCAGCT AATTCACATG CATTATTTTG ATTGTTTTAC AGAATCTGCC ATAAGACAAG
5401 CCATATTAGG ACACATAGTT TTTCTAGGT GTGACTATCA AGCAGGACAT AAGAAGGTAG
5461 GATCTCTGCA ATACTTGGCA CTGACAGCAT TGATAAAACC AAAAAAGAGA AAGCCACCTC
5521 TGCCTAGTGT TAGAAAATTA GTAGAGGATA GATGGAACGA CCCCAGAAG ACCAGGGGCC
5581 GCAGAGGGAA CCATACAATG AATGGACACT AGAGATTCTA GAAGAACTCA AGCAGGAAGC
5641 TGTCAGACAC TTTCTAGAC CATGGCTCCA TAGCTTAGGA CAATATATCT ATGAAACCTA
5701 TGGGGATACT TGGACGGGAG TTGAAGCTAT AATAAGAGTA CTGCAACAAC TACTGTTTCAT
5761 TCATTTTCAGA ATTGATGCC AACATAGCAG AATAGGCATC TTGCGACAGA GAAGAGCAAG
5821 AAATGGAGCC AGTAGATCCT AAATAAAGC CCTGGAACCA TCCAGGAAGC CAACCTAAAA
5881 CAGCTTGTA TAATTGCTTT TGCAAACACT GTAGCTATCA TTGTCTAGTT TGCTTTCAGA
5941 CAAAAGGTTT AGGCATTTCC TATGGCAGGA AGAAGCGGAG ACAGCGACGA AGCGCTCCTC
6001 CAAGTGGTGA AGATCATCAA AATCCTCTAT CAAAGCAGTA AGTACACATA GTAGATGTAA
6061 TGGTAAGTTT AAGTTTATTT AAAGGAGTAG ATTATAGATT AGGAGTAGGA GCATTGATAG
6121 TAGCACTAAT CATAGCAATA ATAGTGTGGA CCATAGCATA TATAGAATAT AGGAAATTTG
6181 TAAGACAAA GAAAATAGAC TGGTTAATTA AAAGAATTAG GGAAAGAGCA GAAGACAGTG
6241 GCAATGAGAG TGATGGGGAC ACAGAAGAAT TGTCAACAAT GGTGGATATG GGGCATCTTA
6301 GGCTTCTGGA TGCTAATGAT TTGTAACACG GAGGACTTGT GGGTCACAGT CTACTATGGG

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FIGURE 1C

6361 GTACCTGTGT GGAGAGAAGC AAAAAGTACT CTATTCTGTG CATCAGATGC TAAAGCATAT
 6421 GAGACAGAAG TGCATAATGT CTGGGCTACA CATGCTTGTG TACCCACAGA CCCCACCCCA
 6481 CAAGAAATAG TTTTGGGAAA TGTAACAGAA AATTTTAATA TGTGGAAAAA TAACATGGCA
 6541 GATCAGATGC ATGAGGATAT AATCAGTTTA TGGGATCAA GCCTAAAGCC ATGTGTAAAG
 6601 TTGACCCAC TCTGTGTCAC TTTAACTGT ACAGATACAA ATGTTACAGG TAATAGAACT
 6661 GTTACAGGTA ATACAAATGA TACCAATATT GCAAATGCTA CATATAAGTA TGAAGAAATG
 6721 AAAAATTGCT CTTTCAATGC AACCACAGAA TTAAGAGATA AGAAACATAA AGAGTATGCA
 6781 CTCTTTTATA AACTTGATAT AGTACCACTT AATGAAAATA GTAACAACCTT TACATATAGA
 6841 TTAATAAATT GCAATACCTC AACCATAACA CAAGCCTGTC CAAAGGTCTC TTTTGACCCG
 6901 ATTCTATAC ATTACTGTGC TCCAGCTGAT TATGCGATT CAAAGTGTAA TAATAAGACA
 6961 TTCAATGGGA CAGGACCATG TTATAATGTC AGCACAGTAC AATGTACACA TGGGAATTAAG
 7021 CCAGTGGTAT CAACTCAACT ACTGTTAAAT GGTAGTCTAG CAGAAGAAGG GATAATAATT
 7081 AGATCTGAAA ATTTGACAGA GAATACCAAA ACAATAATAG TACATCTTAA TGAATCTGTA
 7141 GAGATTAATT GTACAAGGCC CAACAATAAT ACAAGGAAAA GTGTAAGGAT AGGACCAGGA
 7201 CAAGCATTCT ATGCAACAAA TGACGTAATA GGAAACATAA GACAAGCACA TTGTAACATT
 7261 AGTACAGATA GATGGAATAA AACTTTACAA CAGGTAATGA AAAAATTAGG AGAGCATTTC
 7321 CCTAATAAAA CAATAAAATT TGAACCACAT GCAGGAGGGG ATCTAGAAAT TACAATGCAT
 7381 AGCTTTAATT GTAGAGGAGA ATTTTCTAT TGCAATACAT CAAACCTGTT TAATAGTACA
 7441 TACTACCCTA AGAATGGTAC ATACAAATAC AATGGTAATT CAAGCTTACC CATCACACTC
 7501 CAATGCAAAA TAAAACAAAT TGTAAGCATG TGGCAAGGGG TAGGACAAGC AATGTATGCC
 7561 CCTCCCATG CAGGAAACAT AACATGTAGA TCAAACATCA CAGGAATACT ATTGACACGT
 7621 GATGGGGGAT TTAACAACAC AAACAACGAC ACAGAGGAGA CATTACAGACC TGGAGGAGGA
 7681 GATATGAGGG ATAAGTGGAG AAGTGAATTA TATAAATATA AAGTGGTAGA AATTAAGCCA
 7741 TTGGGAATAG CACCCACTAA GGCAAAAAGA AGAGTGGTGC AGAGAAAAAA AAGAGCAGTG
 7801 GGAATAGGAG CTGTGTTCTT TGGGTTCTTG GGAGCAGCAG GAAGCACTAT GGGCGCAGCG
 7861 TCAATAACGC TGACGGTACA GGCCAGACAA CTGTTGTCTG GTATAGTGCA ACAGCAAAGC
 7921 AATTGCTGA AGGCTATAGA GCGCGAACAG CATATGTTGC AACTCACAGT CTGGGGCATT
 7981 AAGCAGCTCC AGGCGAGAGT CCTGGCTATA TAAAGATACC TAAAGGATCA ACAGCTCCTA
 8041 GGGATTTGGG GCTGCTCTGG AAGACTCATC TGCACCACTG CTGTGCCTTG GAAGTCCAGT
 8101 TGGAGTAATA AATCTGAAGC AGATATTTGG GATAACATGA CTTGGATGCA GTGGGATAGA
 8161 GAAATTAATA ATTACACAGA AACAATATTC AGGTTGCTTG AAGACTCGCA AAACCAGCAG
 8221 GAAAAGAATG AAAAAGATTT ATTAGAATTG GACAAGTGGA ATAATCTGTG GAATTGGTTT
 8281 GACATATCAA ACTGGCTGTG GTATATAAAA ATATTCATAA TGATAGTAGG AGGCTTGATA
 8341 GGTTTAAGAA TAATTTTTCG TGTCCTCTCT ATAGTGAATA GAGTTAGGCA GGGATACTCA
 8401 CCTTTGTCAT TTCAGACCCT TACCCCAAGC CCGAGGGGAC TCGACAGGCT CGGAGGAATC
 8461 GAAGAAGAAG GTGGAGAGCA AGACAGAGAC AGATCCATAC GATTGGTGAG CGGATTCTTG
 8521 TCGCTTGCCCT GGGACGATCT GCGGAGCCTG TGCCCTCTTCA GCTACCACCG CTTGAGAGAC
 8581 TTCATATTAA TTGCAGTGAG GGCAGTGGAA CTTCTGGGAC ACAGCAGTCT CAGGGGACTA
 8641 CAGAGGGGGT GGGAGATCCT TAAGTATCTG GGAAGTCTTG TGCAGTATTG GGGTCTAGAG
 8701 CTAAAAAAGA GTGCTATTAG TCCGCTTGAT ACCATAGCAA TAGCAGTAGC TGAAGGAACA
 8761 GATAGGATTA TAGAATTGGT ACAGAAGAATT TGTAGAGCTA TCCTCAACAT ACCTAGGAGA
 8821 ATAAGACAGG GCTTTGAAGC AGCTTTGCTA TAAAATGGGA GGCAAGTGGT CAAAACGCAG
 8881 CATAGTTGGA TGGCCTGCAG TAAGAGAAAG AATGAGAAGA ACTGAGCCAG CAGCAGAGGG
 8941 AGTAGGAGCA GCGTCTCAAG ACTTAGATAG ACATGGGGCA CTTACAAGCA GCAACACACC
 9001 TGCTACTAAT GAAGCTTGTG CCTGGCTGCA AGCACAAGAG GAGGACGGAG ATGTAGGCTT
 9061 TCCAGTCAGA CCTCAGGTAC CTTTAAGACC AATGACTTAT AAGAGTGCAG TAGATCTCAG
 9121 CTTCTTTTAA AAAGAAAAGG GGGGACTGGA AGGGTTAATT TACTCTAGGA AAAGGCAAGA
 9181 AATCCTTGAT TTGTGGGTCT ATAACACACA AGGCTTCTTC CCTGATTGGC AAAACTACAC
 9241 ATCGGGGCCA GGGGTCCGAT TCCCACTGAC CTTTGGATGG TGCTTCAAGC TAGTACCAGT
 9301 TGACCCAAGG GAGGTGAAAG AGGCCAATGA AGGAGAAGAC AACTGTTTGC TACACCCTAT
 9361 GAGCCAACAT GGAGCAGAGG ATGAAGATAG AGAAGTATTA AAGTGGAAAG TTGACAGCCT
 9421 TCTAGCACAC AGACACATGG CCCGCGAGCT ACATCCGGAG TATTACAAAG ACTGCTGACA

FIGURE 1D

9481 CAGAAGGGAC TTTCCGCCTG GGACTTTCCA CTGGGGCGTT CCGGGAGGTG TGGTCTGGGC
 9541 GGGACTTGGG AGTGGTCACC CTCAGATGCT GCATATAAGC AGCTGCTTTT CGCTTGTAAT
 9601 GGGTCTCTCT CGGTAGACCA GATCTGAGCC TGGGAGCTCT CTGGCTATCT AGGGAACCCA
 9661 CTGCTTAGGC CTCATAAAG CTTGCCCTGA GTGCTCTAAG TAGTGTGTGC CCATCTGTTG
 9721 TGTGACTCTG GTAACAGAG ATCCCTCAGA CCCTTTGTGG TAGTGTGGAA AATCTCTAGC
 9781 A

Figure 2A

↓: indicates the regions for β -sheet and V1/V2 loop deletions

*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N → Q) or deletions can be performed.

		1		50
B-SF162	(1)	----MDAMKRGLCCLLCDAVFSP-SAVEK	WVTVYYGVPV	EAATT
C-TV1.8_2	(1)	MTQCCQ	WVTVYYGVPV	EAATT
C-TV1.8_5	(1)	MTQCCQ	WVTVYYGVPV	EAATT
C-TV2.12-5/1	(1)	ARILLYRH	WVTVYYGVPV	EAATT
C-MJ4	(1)	KGIPWQ	WVTVYYGVPV	EAATT
IndiaC-93IN101	(1)	RTILYQ	WVTVYYGVPV	EAATT
A-Q2317	(1)	MGIOQC	WVTVYYGVPV	EAATT
D-92UG001	(1)	REIEEYLCL	WVTVYYGVPV	EAATT
E-cm235	(1)	----MDAMKRGLCCLLCDAVFSP-SASNN	WVTVYYGVPV	EAATT
Consensus	(1)	MRV G RN Q WWI	GILGFWMLM S E	LWVTVYYGVPVWREAKTT
		51		100
B-SF162	(46)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
C-TV1.8_2	(50)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
C-TV1.8_5	(50)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
C-TV2.12-5/1	(50)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
C-MJ4	(49)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
IndiaC-93IN101	(51)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
A-Q2317	(51)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
D-92UG001	(51)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
E-cm235	(46)	LFCASDAK	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
Consensus	(51)	LFCASDAKAYETEVHNV	WATHACVPTDPNP	EIVLNVTEFNMWNNMM
		101		150
B-SF162	(96)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
C-TV1.8_2	(100)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
C-TV1.8_5	(100)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
C-TV2.12-5/1	(100)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
C-MJ4	(99)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
IndiaC-93IN101	(101)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
A-Q2317	(101)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
D-92UG001	(101)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
E-cm235	(96)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
Consensus	(101)	EQMHEDI	ISLWDQSLKPCVKLTPLCVTLNCT	NTNNTN
		151		200
B-SF162	(138)	NWKEMDRGE	KNCSFNT	TKKQYALFYLDV
C-TV1.8_2	(150)	GIYNI	KNCSFNT	TKKQYALFYLDV
C-TV1.8_5	(150)	ANATYKY	KNCSFNT	TKKQYALFYLDV
C-TV2.12-5/1	(141)	-----K	KNCSFY	TKKQYALFYLDV
C-MJ4	(139)	TNAEMKA	KNCSFY	TKKQYALFYLDV
IndiaC-93IN101	(141)	NYNGSV	KNCSFY	TKKQYALFYLDV
A-Q2317	(139)	-G--DR	KNCSFY	TKKQYALFYLDV
D-92UG001	(144)	GMENNDQ	KNCSFY	TKKQYALFYLDV
E-cm235	(141)	NIIGNIT	KNCSFY	TKKQYALFYLDV
Consensus	(151)	T	EEMKNCSFNITELRDKK	KEYALFYKLDIVELN N N S

Figure 2B

	201	*		*	*	250
B-SF162	(183)	SYRLINCA	NTSVITQ	CPKVSF	PIPIHYCAPAGY	ILKCNDRKFNNGGEC
C-TV1.8_2	(197)	TYRLINCA	NTSTITQ	CPKVSF	PIPIHYCAPAGY	ILKCNDRKFNNGGEC
C-TV1.8_5	(197)	TYRLINCA	NTSTITQ	CPKVSF	PIPIHYCAPAGY	ILKCNDRKFNNGGEC
C-TV2.12-5/1	(183)	NYRLINCA	NTSAITQ	CPKVSF	PIPIHYCAPAGY	PLKCNDRKFNNGGEC
C-MJ4	(189)	EYRLINCA	DTSTITQ	CPKVSF	PIPIHYCAPAGY	ILKCNDRKFNNGGEC
IndiaC-93IN101	(191)	EYRLINCA	NTSAITQ	CPKVSF	PIPIHYCAPAGY	ILKCNDRKFNNGGEC
A-Q2317	(182)	EYRLINCA	NTSAITQ	CPKVSF	PIPIHYCAPAGY	ILKCKDEGFNGIGLC
D-92UG001	(194)	NYRLINCA	NTSAITQ	CPKVSF	PIPIHYCAPAGY	ILKCRDRKFNNGGEC
E-cm235	(188)	EYRLINCA	NTSVIKQ	CPKVSF	PIPIHYCAPAGY	ILKCNDRKFNNGGEC
Consensus	(201)	YRLINCNTS	ITQACPKVSF	PIPIHYCAPAGY	AILKCNDRKFNNGGEC	
	251	*		*	*	300
B-SF162	(233)	TNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTDNAKIIVQLK
C-TV1.8_2	(247)	YNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTENTKTIIVHLN
C-TV1.8_5	(247)	YNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTENTKTIIVHLN
C-TV2.12-5/1	(233)	DNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTNVKTIIVHLN
C-MJ4	(239)	NNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTDNVKTIVHLN
IndiaC-93IN101	(241)	NNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTNVKTIIVHLN
A-Q2317	(232)	KNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTNAKTIIVQLV
D-92UG001	(244)	KNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTNAKTIIVQLV
E-cm235	(238)	KNVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTNAKTIIVHLN
Consensus	(251)	NVSVQC	THGIRP	PVVSTQ	LLNGSLAEEG	IIIRSENFTNN KTIIVHLN
	301	*		*	*	350
B-SF162	(283)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
C-TV1.8_2	(297)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
C-TV1.8_5	(297)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
C-TV2.12-5/1	(283)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
C-MJ4	(289)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
IndiaC-93IN101	(291)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
A-Q2317	(282)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
D-92UG001	(294)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
E-cm235	(288)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
Consensus	(301)	ESVEINCT	RPN-NNTRK	SIRIGPGQAFYATGDI	IGDIRQAHCNIS	KWN
	351	*		*	*	400
B-SF162	(332)	NTLQV	VTKLQAFG	NKT-IVFKQ	SGGDPEIVMHS	FNCGGEFFYCNS
C-TV1.8_2	(346)	NTLQV	MKKLGEH	FPPKT-IQFKQ	SGGDPEIVMHS	FNCGGEFFYCNS
C-TV1.8_5	(346)	NTLQV	MKKLGEH	FPPKT-IQFKQ	SGGDPEIVMHS	FNCGGEFFYCNS
C-TV2.12-5/1	(332)	NTLQV	SQKLQELFP	STGIKFAH	SGGDPEIVMHS	FNCGGEFFYCNS
C-MJ4	(338)	NTLQV	SEKLGEH	FPPKT-IQFDQ	PIGGDPEIVMHS	FNCGGEFFYCNS
IndiaC-93IN101	(340)	NTLQV	GKKLGEH	FPPKT-IKFAS	SGGDPEIVMHS	FNCGGEFFYCNS
A-Q2317	(331)	NTLQV	AEKLRT	IFGNT-IIFANS	SGGDPEIVMHS	FNCGGEFFYCNS
D-92UG001	(343)	NTLQV	AKKLGLFN	TT-IIFKS	SGGDPEIVMHS	FNCGGEFFYCNS
E-cm235	(337)	NTLQV	TEKLGEH	FPPKT-IIFQ	SGGDPEIVMHS	FNCGGEFFYCNS
Consensus	(351)	NTLQV	KL EHF	NKT I F P	SGGDLEITTHS	FNCGGEFFYCNS

Figure 2C

		401		*		*		820/821	↓	500	
B-SF162	(381)	LFN	STNN	---	TIGPN	---	TGII	PCRIKQIINMWQVGGRAMYAPP			
C-TV1.8_2	(395)	LFN	STHS	---	NQYKY	GNSSSPI	QCC	IKQIINMWQVGQATYAPP			
C-TV1.8_5	(395)	LFN	STYP	---	KQYKY	GNSSLPI	QCC	IKQIINMWQVGQATYAPP			
C-TV2.12-5/1	(382)	LFN	ST	SNGTCT	CM	---	NTERI	QCCRIKQIINMWQVGQATYAPP			
C-MJ4	(387)	LFN	STNS	---	TGDT	---	SH	ISCHRIKQIINMWQVGQATYAPP			
IndiaC-93IN101	(389)	LFN	ST	MPTYM	TESNS	---	NS	ITECRIKQIINMWQVGQATYAPP			
A-Q2317	(380)	LFN	ST	YVNSTW	DST	---	ESND	ITECRIKQIINMWQVGQATYAPP			
D-92UG001	(392)	LFN	ST	AND	STW	IGNNNTGSD	NE	ITECRIKQIINMWQVGQATYAPP			
E-cm235	(386)	LFN	ST	ICIE	---	NG	MGGC	---	NG	ITILPCRIKQIINMWQVGQATYAPP	
Consensus	(401)	LFN	STY		NGT	N	N	TITLPCRIKQIINMWQVGGRAMYAPP			
		451	*	*	*	*				500	
B-SF162	(424)	IRG	ST	IRCSSNITG	LL	DGGKE	NT	---	TEIFRP	GGG	MDNWRSELY
C-TV1.8_2	(442)	IRG	ST	IRCSNITG	LL	DGGFNT	NT	---	TEIFRP	GGG	MDNWRSELY
C-TV1.8_5	(442)	IRG	ST	IRCSNITG	LL	DGGFNT	NT	---	TEIFRP	GGG	MDNWRSELY
C-TV2.12-5/1	(430)	IRG	ST	IRCSNITG	LL	DGGDN	ET	---	EIFRP	GGG	MDNWRSELY
C-MJ4	(428)	IRG	ST	IRCKSNITG	LL	DGGNET	GI	---	EIFRP	GGG	MDNWRSELY
IndiaC-93IN101	(436)	IRG	ST	IRCTSNITG	LL	VHOGGIKEND	TENKTE	IFRP	GGG	MDNWRSELY	
A-Q2317	(429)	IPG	VIKCESNITG	LL	DGGKD	NV	---	---	EIFRP	GGG	MDNWRSELY
D-92UG001	(441)	IEG	WINCASNITG	LL	DGGGAND	S	---	---	NEIFRP	GGG	MDNWRSELY
E-cm235	(429)	IEG	RINCVSNITG	LL	DGGAIN	IT	---	---	EIFRP	GGG	MDNWRSELY
Consensus	(451)	IAG	NITC	SNITG	LL	TRDGG	NT	N	ETFRP	GGG	MDNWRSELY
		501									550
B-SF162	(471)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
C-TV1.8_2	(489)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
C-TV1.8_5	(491)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
C-TV2.12-5/1	(476)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
C-MJ4	(474)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
IndiaC-93IN101	(486)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
A-Q2317	(475)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
D-92UG001	(488)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
E-cm235	(475)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
Consensus	(501)	KYK	VV	KIEPLG	APT	KRRV	VOREKRA	VG	IFG	FLGAAGSTMGAAS	
		551									600
B-SF162	(521)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
C-TV1.8_2	(539)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
C-TV1.8_5	(541)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
C-TV2.12-5/1	(526)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
C-MJ4	(524)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
IndiaC-93IN101	(536)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
A-Q2317	(525)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
D-92UG001	(538)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
E-cm235	(525)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE
Consensus	(551)	ITLT	V	QARQLLSGIV	Q	SNLL	RAIEAQQH	LL	QLT	VWG	IKQLOARVLAVE

Figure 2D

	601		650
B-SF162	(571)	RYLKDOQLLGWGCSEICTTAVWNSSWSNKSLDQIWNNTWMEWRE	
C-TV1.8_2	(589)	RYLKDOQLLGWGCSEICTTAVWNSSWSNKSEKIWNNTWMEWRE	
C-TV1.8_5	(591)	RYLKDOQLLGWGCSEICTTAVWNSSWSNKEAIWNNTWMEWRE	
C-TV2.12-5/1	(576)	RYLQDQQLLGWGCSEICTTNVLWNSSWSNKQSIWNNTWMEWRE	
C-MJ4	(574)	RYLKDOQLLGWGCSEICTTAVWNSSWSNQHAIWNNTWMEWRE	
IndiaC-93IN101	(586)	RYLKDOQLLGWGCSEICTTAVWNSSWSNKQSIWNNTWMEWRE	
A-Q2317	(575)	RYLKDOQLLGWGCSEICTTNVLWNSSWSNKSLDIWNNTWMEWRE	
D-92UG001	(588)	RYLQDQQLLGWGCSEHICTTAVWNSSWSNKIDAIWNNTWMEWRE	
E-cm235	(575)	RYLKDOQLLGWGCSEICTTAVWNSSWSNYESAIWNNTWMEWRE	
Consensus	(601)	RYLKDOQLLGWGCSEKICTTAVPNSSWSNKS DIWNNTWMEWRE	
	651		700
B-SF162	(621)	ISNYTGLIIRLLEESONQOEKNEKLLLELDKRWASLWNWFSIKWYIKI	
C-TV1.8_2	(639)	ISNYTGLIIRLLEESONQOEKNEKLLLELDKRWNLWNWFSIKWYIKI	
C-TV1.8_5	(641)	ISNYTGLIIRLLEESONQOEKNEKLLLELDKRWNLWNWFSIKWYIKI	
C-TV2.12-5/1	(626)	ISNYTGLIIRLLEESONQOEKNEKLLALDKNLWNWFSIKWYIKI	
C-MJ4	(624)	ISNYTGLIIRLLEESONQOEKNEKLLALDSWKTLWSWFSIKWYIKI	
IndiaC-93IN101	(636)	ISNYTGLIIRLLEESONQOEKNEKLLALDSWKTLWSWFSIKWYIKI	
A-Q2317	(625)	ISNYTGLIIRLLEESONQOEKNEKLLLELDKRWNLWNWFSIKWYIKI	
D-92UG001	(638)	ISNYTGLIIRLLEESONQOEKNEKLLLELDKRWNLWNWFSIKWYIKI	
E-cm235	(625)	ISNYTGLIIRLLEESONQOEKNEKLLLELDKRWNLWNWFSIKWYIKI	
Consensus	(651)	ISNYTGLIIRLLEESONQOEKNEKLLLELDKRWNLWNWFSIKWYIKI	
	701		750
B-SF162	(671)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTRFPAARRDRPDRIE	
C-TV1.8_2	(689)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
C-TV1.8_5	(691)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
C-TV2.12-5/1	(676)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
C-MJ4	(674)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
IndiaC-93IN101	(686)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
A-Q2317	(675)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
D-92UG001	(688)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
E-cm235	(675)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
Consensus	(701)	FIMIVGGLIGLRIFFVLSTVNRVRQGYSPLSQTHLPAARRDRPDRIE	
	751		800
B-SF162	(721)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
C-TV1.8_2	(739)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
C-TV1.8_5	(741)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
C-TV2.12-5/1	(726)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
C-MJ4	(724)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
IndiaC-93IN101	(736)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
A-Q2317	(725)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
D-92UG001	(738)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
E-cm235	(725)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	
Consensus	(751)	EEGGEQDRSRIRLVSGFLALAWDDLRLCLFSEYHRLRDLIFIAARVEL	

Figure 2E

	801	850
B-SF162	(771) LGH-----RGWEALKYWNLQYWIQELKNSAIFDAAIAVAEGTD	
C-TV1.8_2	(789) LGHSSDTHQGWIDIKYIGSLQYWGDELKSSNGLISDAITVAEGTD	
C-TV1.8_5	(791) LGHSSDTHQGWIDIKYIGSLQYWGDELKSSNGLISDAITVAEGTD	
C-TV2.12-5/1	(776) LGHSSDTHQGWIDIKYIGSLQYWGDELKSSNGLISDAITVAEGTD	
C-MJ4	(774) LGHSSDTHQGWIDIKYIGSLQYWGDELKSSNGLISDAITVAEGTD	
IndiaC-93IN101	(786) LGHSSDTHQGWIDIKYIGSLQYWGDELKSSNGLISDAITVAEGTD	
A-Q2317	(775) LGHSSDTHQGWIDIKYIGSLQYWGDELKSSNGLISDAITVAEGTD	
D-92UG001	(788) LGH-----RGWEALKYWNLQYWGDELKSSNGLISDAITVAEGTD	
E-cm235	(775) LGHSSDTHQGWIDIKYIGSLQYWGDELKSSNGLISDAITVAEGTD	
Consensus	(801) LGRSSLRGL RGWEALKYLGSLQYWGDELKSSAISLLDTIAIAVAEGTD	

	851	879
B-SF162	(814) RRIELVQRI RAILNIPRRIRQGLERTLL	
C-TV1.8_2	(839) RRIELVQRI RAILNIPRRIRQGLERTLL	
C-TV1.8_5	(841) RRIELVQRI RAILNIPRRIRQGLERTLL	
C-TV2.12-5/1	(826) RRIELVQRI RAILNIPRRIRQGLERTLL	
C-MJ4	(824) RRIELVQRI RAILNIPRRIRQGLERTLL	
IndiaC-93IN101	(829) RRIELVQRI RAILNIPRRIRQGLERTLL	
A-Q2317	(825) RRIELVQRI RAILNIPRRIRQGLERTLL	
D-92UG001	(831) RRIELVQRI RAILNIPRRIRQGLERTLL	
E-cm235	(825) RRIELVQRI RAILNIPRRIRQGLERTLL	
Consensus	(851) RRIELVQRI RAILNIPRRIRQGLERTLL	

Figure 3

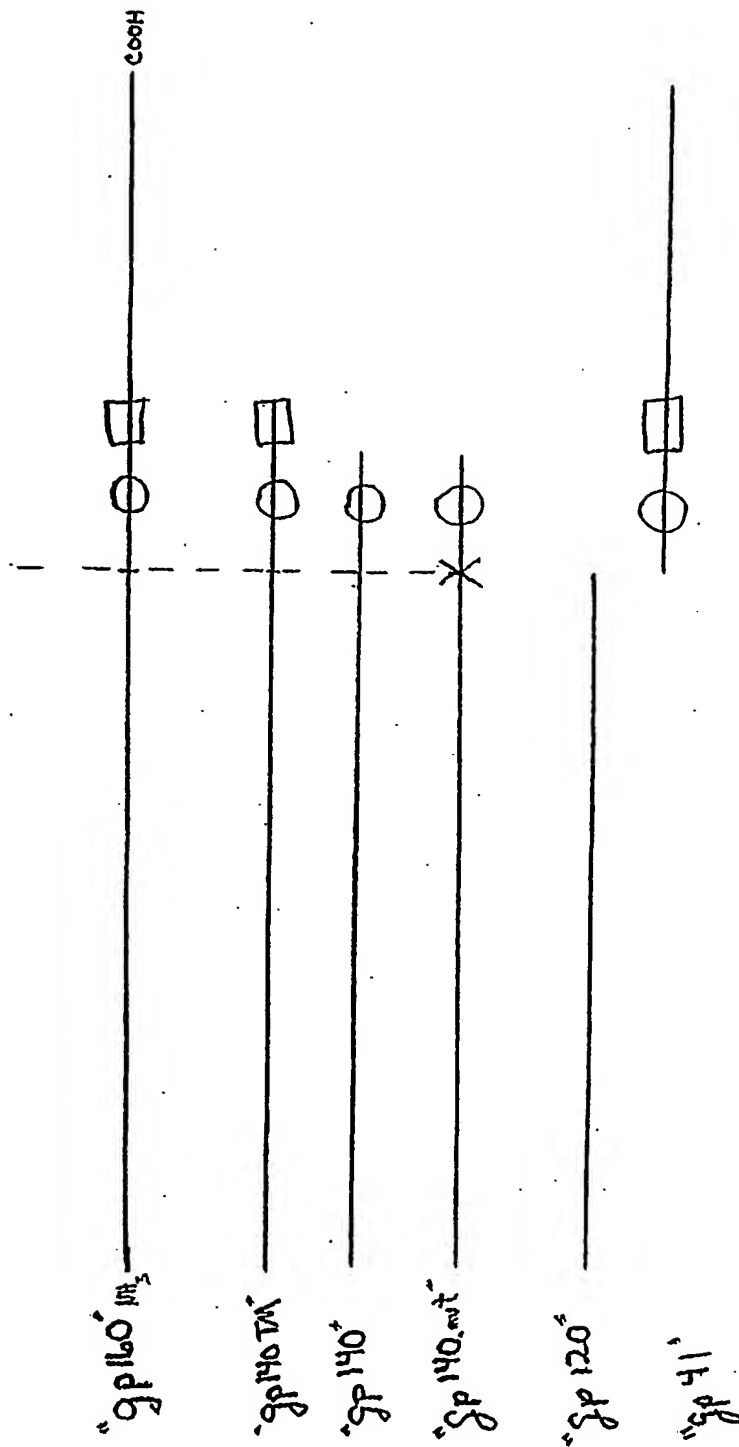


Figure 4

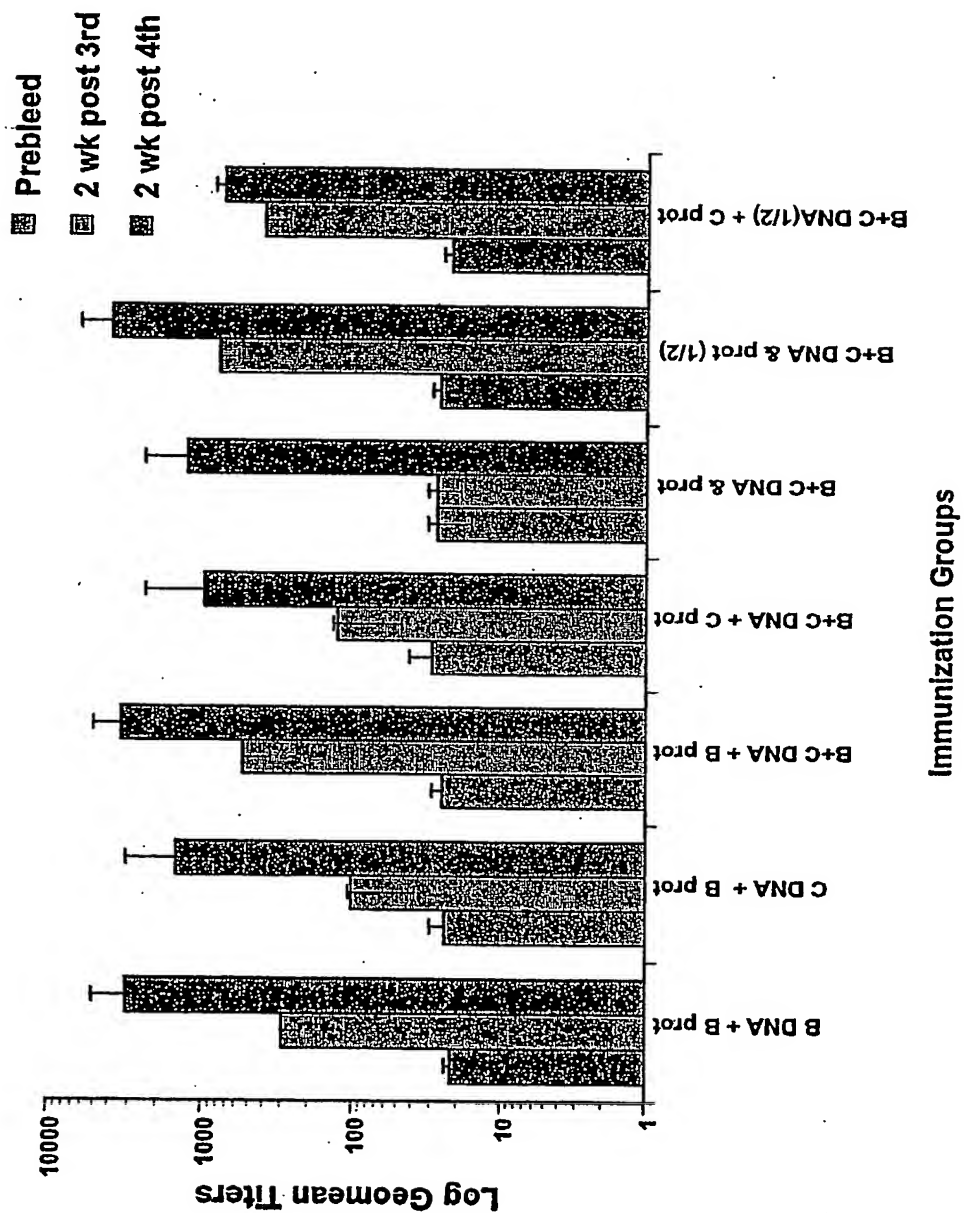
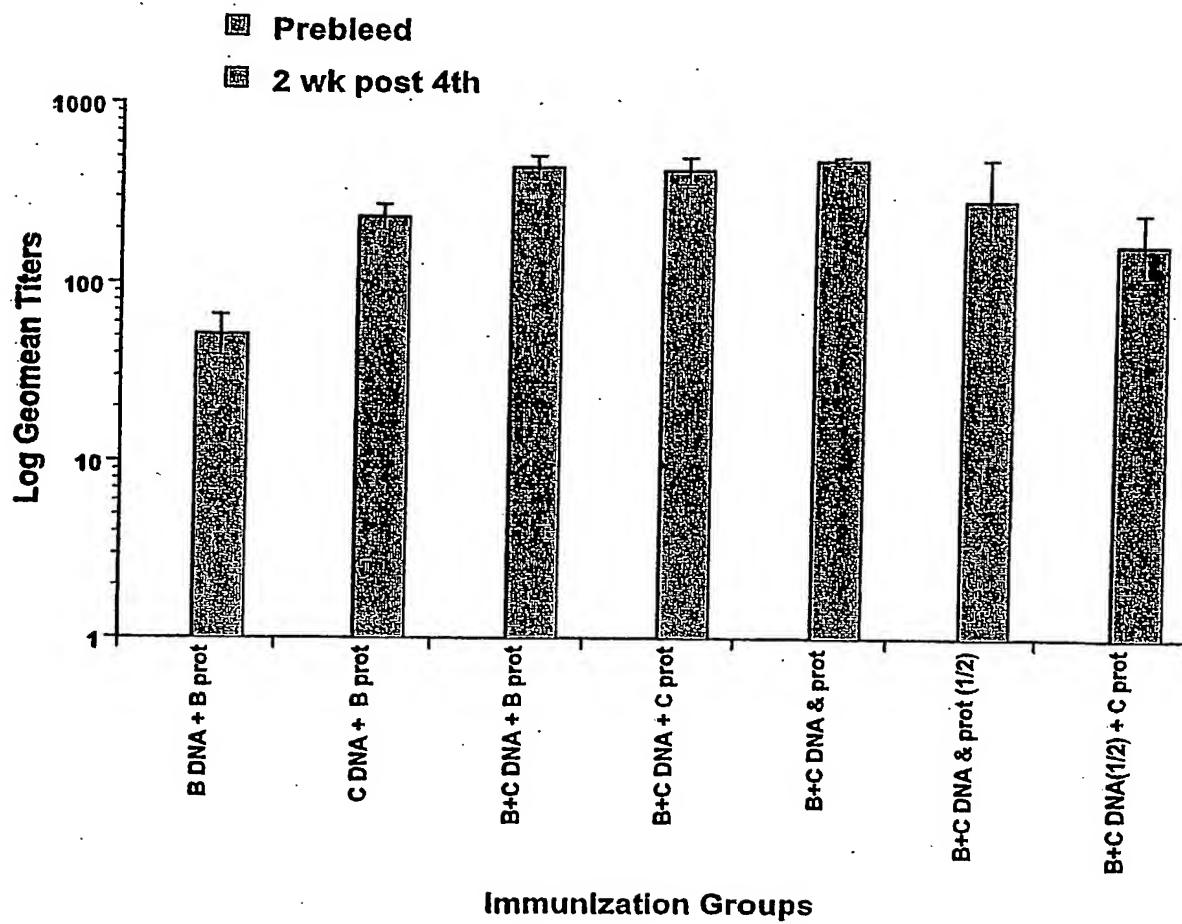


Figure 5

gp140.modSF162.delV2

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Figure 6

gp140.mut7.modSF162.delV2

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Figure 7

gp140mod.TV1.delV2

```

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1141  aagtacaacg gcaacagcag cagcccacac accctgcagt gcaagatcaa gcagatcgtg
1201  cgcattgtggc agggcgtggg ccaggccacc tacgcccccc ccactgcggg caacatcacc
1261  tgccgcagca acatcaocgg catcctgctg acccgcgacg ggggttcaa caccaccaac
1321  aacaccgaga ccttcogccc ogggcgcggc gacatgcgcg acaactggcg cagcagatg
1381  tacaagtaca aggtggtgga gatcaagccc ctgggcatcg cccccaccaa ggccaagcgc
1441  cgcgtggtgc agcgcgagaa gcgcgcgctg ggcatcggcg ccgtgttcct gggottcctg
1501  ggcgcgcgcg gcagcaccat gggcgcgcc agcatcacc tgacocgtga ggcccgccag
1561  ctgctgagcg gcatcgtgca gcagcagagc aacctgctga aggccatcga ggcccgagc
1621  cacatgctgc agctgaccgt gtggggcatc aagcagctgc aggcocgcgt gctggccatc
1681  gagcgctacc tgaaggacca gcagctgctg ggcactctgg gctgcagcgg ccgootgatc
1741  tgacccaocg ccgtgocctg gaacagcagc tggagcaaca agagcgagaa ggacatctgg
1801  gacaacatga cctggatgca gtgggaocgc gagatcagca actacaccgg cctgatctac
1861  aacctgctgg aggcagacca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921  gacaagtgga acaacctgtg gaactggttc gacatcagca actggccctg gtacatctaa
1981  ctogag

```

Figure 8

gp140mod.TV1.mut7.delV2

1 gaattcatgc gogtgatggg caccagaag aactgcoago agtgggtggat ctgggggaatc
 61 ctgggcttct ggatgtgat gatotgcaa acogaggaco tgggggtgao ogtgtactac
 121 ggcgtgccog tggggogoga ogccaagacc acctgttct gogooagoga ogccaaggcc
 181 taogagaccg aggtgoacaa ogtgtgggc accoagoot gogtgocao ogacccaac
 241 ccocaggaga tctgtctggg caaogtgacc gagaacttca acatgtggaa gaacgacatg
 301 gcogaccaga tgcacgagga ogtgatcagc ctgtgggao agagootgaa gccotgcgtg
 361 aagctgacco cctgtgcgt gacctgaac tgcacgaca ocaogtgao oggoaacogo
 421 acogtgaccg goaacagcao caacaacacc aoggoaccg gcatctcaa catogaggag
 481 atgaagaact goagcttcaa ogcgggcgo ggoogootga toaactgaa caccagcaco
 541 ataccocagg cctgcccac ggtgagcttc gacccatco ccatocata ctgcctccc
 601 gcoggtctag ccatctgaa gtgcaacaac aagaccttca acggcaccgg cccctgtac
 661 aaogtgagca cogtgcatg caccacggc atcaagccog tggtagcao coagctgtg
 721 ctgaacggca gcctggccga ggagggcac atcatccga gogagaacct gaccgagaa
 781 accaagacca tcatctgca ctgaacgag agogtgaga tcaactgac cggcccaac
 841 aacaacacc gcaagagcgt gogcatggc ccgggcagg ccttctacg caccaagac
 901 gtgatoggca acatccgca ggcctactgc aacatcagca ccgaccgtg gaacaagacc
 961 ctgacgagg tcatgaaga gctgggogag cacttccca acaagaccat coagttcaag
 1021 cccacogcg gcggcgacct ggagatcac atgcacagct tcaactgoc oggogagtic
 1081 ttctactgca acaccagca cctgttcaac agcacctacc acagcaaca cggcacctac
 1141 aagtaaacg gcaacagcag cagcccatc acctgcagt goagatcaa gcagatcgtg
 1201 ogcatgtggc agggcgtggg ccaggccaco tacgcccccc ccatgcogg caaatcaco
 1261 tggcgagca acatccogg catctgtg accogcagc ggggttcaa caocaccaac
 1321 aacaccgaga ccttcggcc ogcgggcggc gacatgcgc acaactggcg cagcgagctg
 1381 tacaagtaca aggtggtgga gatcaagccc ctgggoatog ccccaacca ggcatcagc
 1441 agcgtggtgc agagcgagaa gagcgccgtg ggcatoggcg cctgttctt gggcttcctg
 1501 ggcgcggcg gcagcaccat gggcgccgc agoatcccc tgacctgca ggccggccag
 1561 ctgttgagcg gcatctgca gcagcagagc aacctgtga aggcacoga ggccagcag
 1621 cacatgtgc agctgacct gtggggcatc aagcagctgc aggcgcgct gctggccatc
 1681 gagcgctacc tgaaggacca gcagctgtg ggcatotggg gctgcagcg ccgctgato
 1741 tgcaccaacc cgtgcccctg gaacagcagc tggagcaaca agagogagaa ggacatctg
 1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccg cctgatctac
 1861 aacctgtgg aggcagcca gaaccagcag gagaagaac agaaggacct gctggagctg
 1921 gacaagtgga acaacctgtg gaactgttc gacatcagca actggccctg gtacatctaa
 1981 ctogag

Figure 9

FIGURE 10
gp160mod.Q23-17

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1 ATGCGCGTGA TGGGCATCCA GCGCAACTGC CAGCACCTGC TGACCTGGGG CATCATGATC
61 CTGGGCACCA TCATCTTCTG CAGCGCCGTG GAGAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCGTGT GGCGCGACGC CGACACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
181 GAGACCGAGA AGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCACCC
241 CAGGAGATCC ACCTGGACAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAA
361 CTGACCCCCC TGTGCGTGAC CCTGCACTGC ACCAACGTGA CCAGCGTGAA CACCACCGGC
421 GACCGCGAGG GCCTGAAGAA CTGCAGCTTC AACATGACCA CCGAGCTGCG CGACAAGCGC
481 CAGAAGGTGT ACAGCCTGTT CTACCGCCTG GACATCGTGC CCATCAACGA GAACCAGGGC
541 AGCGAGTACC GCCTGATCAA CTGCAACACC AGCGCCATCA CCCAGGCTG CCCCAGGTG
601 AGCTTCGAGC CCATCCCCAT CCACTACTGC ACCCCGCGCG GCTTCGCCAT CCTGAAGTGC
661 AAGGACGAGG GCTTCAACGG CACCGGCGCTG TGCAAGAAGC TGAGCACCCT GCAGTGCACC
721 CACGGCATCA AGCCCGTGGT GAGCACCAG CTGCTGCTGA ACGGCAGCCT GGCCGAGAAG
781 AACATCACCA TCCGCAGCGA GAACATCACC AACAAACGCA AGATCATCAT CGTGCGCTG
841 GTGCAGCCCG TGACCATCAA GTGCATCCGC CCCAACAAAC ACACCCGCAA GAGCATCCGC
901 ATCGGCCCCG GCCAGGCCCT CTACGCCACC GCGCAGATCA TCGGCGACAT CCGCCAGGCC
961 CACTGCAACG TGACCCGCGC CCGCTGGAAC AAGACCCTGC AGGAGGTGGC CGAGAAGCTG
1021 CGCACCTACT TCGGCAACAA GACCATCATC TTCGCCAACA GCAGCGCGCG CGACCTGGAG
1081 ATCACCACCC ACAGCTTCAA CTGCGGCGGC GAGTTCTTCT ACTGCAACAC CAGCGGCTG
1141 TTCAACAGCA CCTGGTACGT GAACAGCACC TGGAACGACA CCGACAGCAC CCAGGAGAGC
1201 AACGACACCA TCACCCTGCC CTGCCGCATC AAGCAGATCA TCAACATGTG GCAGCGCGCC
1261 GGCCAGGCCA TGTACGCCCC CCCCATCCCC GGCGTGATCA AGTGCGAGAG CAACATCACC
1321 GGCTGCTGCG TGACCCGCGA CGGCGGCAAG GACAACAACG TGAACGAGAC CTTCCGCCCC
1381 GGCGGCGGCG ACATGCGCGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGGAG
1441 ATCGAGCCCC TGGGCGTGCG CCCCACCGCG GCCAAGCGCC GCGTGGTGGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CGTGTTCTTG GGCTTCTTGG GCGCCGCGCG CAGCACCATG
1561 GGCGCCACCA GCATCACCTT GACCGTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAACA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGAA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GCGCGACCAG
1741 CAGCTGCTGG GCATCTGGGG CTGCAGCGGC AAGCTGATCT GCACCACCAA CGTGCCCTGG
1801 AACAGCAGCT GGAGCAACAA GAGCCTGGAC GAGATCTGGA ACAACATGAC CTGGCTGCAG
1861 TGGGACAAGG AGATCAACAA CTACCCCAG CTGATCTACC GCCTGATCGA GGAGAGCCAG
1921 AACCAGCAGG AGAAGAACGA GAAGGAGCTG CTGGAGCTGG ACAAGTGGGC CAACCTGTGG
1981 AGCTGGTTTC ACATCAGCAA CTGGCTGTGG TACATCAAGA TCTTCATCAT CATCGTGGGC
2041 GGCTGATCGC GCCTGCGCAT CGTGTTTCGCC GTGTGAGCG TGATCAACCG CGTGCGCCAG
2101 GGCTACAGCC CCCTGAGCTT CCAGACCCAG ACCCCCAACC CCCGCGGCTT GGACCGCCCC
2161 GAGCGCATCG AGGAGGAGGA CGGCGAGCAG GGCCGCGGCC GCAGCATCCG CCTGGTGAGC
2221 GGCTTCTTGG CCCTGGCCTG GGACGACCTG CGCAGCCTGT GCCTGTTTCA CTACCACGCG
2281 CTGCGCGACT TCATCCTGAT CGCCGCCCCG ACCGTGGAGC TGCTGGGCCA CAGCAGCCTG
2341 AAGGGCCTGC GCCTGGGCTG GGAGGGCATC AAGTACCTGT GGAACCTGCT GAGCTACTGG
2401 GGCCGCGAGC TGAAGATCAG CGCCATCAAC CTGGTGAGCA CCATCGCCAT CGCCGTGGCC
2461 GGCTGGACCG ACCGCGTGAT CGAGATCGCC CAGCGCATCG GCCGCGCAT CCTGCACATC
2521 CCCGTGCGCA TCCGCCAGGG CCTGGAGCGC GCCCTGCTGT AA

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FIGURE 11

gp160mod.98UA0116

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1  ATGAAGGCCC GCGGCATGCA GCGCAACTAC CAGCACCTGT GGCCTGGGG.CACCATGCTG
61  TTCTGGATGA TCATCATGTG CAAGGCCGCC GAGAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCGTGT GGC GCGACGC CGAGACACCC CTGTTCTGCG CCAGCGACGC CAAGGCCCTAC
181 GACAAGGAGG TGCACAACGT GTGGGCCACC CACGCTGCG TGGCCACCGA CCCCAGCCCC
241 CAGGAGATCA TCCTGGAGAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC AGACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC GCCGGCCCCA GCAGCAACAA CAGCAACGTG
421 AACAGCAACA GCAACGACAA CTGGAGCGAG GAGATGAAGA ACTGCAGCTT CAACATGACC
481 ACCGAGCTGC GCGACAAGCG CAAGACCGTG CACAGCCTGT TCTACAAGCT GGACATCGTG
541 AGCACCGGCA GCAACGACAG CCGCCAGTAC CGCTGATCA ACTGCAACAC CAGCGCCATG
601 ACCCAGGCCT GCCCAAGGT GACCTTCGAG CCCATCCCCA TCCACTACTG CGCCCCCGCC
661 GGCTTCGCCA TCCTGAAGTG CAAGGACACC AACTTCACCG GCACCGGCCC CTGCAAGGAC
721 GTGAGCACCG TGCAGTGAC CCACGGCACC AAGCCCGTGG TGAGCACCCA GCTGCTGCTG
781 AACGGCAGCC TGGCCGAGAA GGAGGTGATG ATCCGCAGCG AGAACATCAC CGACAACGGC
841 AAGATCATCA TCGTGCACTG GACCGAGCCC GTGAACATCA CCCGCATCCG CCCC GGCGAG
901 AACAAGCGCA CCAGCATCCG CATCGGCCCC GGCCAGACCT TCTACGCCAC CGGCGACGTG
961 ATCGGCGACA TCCGCAAGGC CTACTGCAAC GTGAGCCGCG CCGCTGGAA CAGCACCTG
1021 CAGAAGATCA GCACCCAGCT GCGCCAGTAC TTCAACAACA AGACCATCAT CTTCAGAAGC
1081 AGCAGCGGCG GCGACCTGGA GGTGACCACC CACAGCTTCA ACTGCGGCGG CGAGTTCTTC
1141 TACTGCAACA CCACCGACCT GTTCAACAGC ACCTGGAAAG AGCACGGCCC CTGACCAAC
1201 AGCACCATGG CCAACGGCAC CATCACCTG CCCTGCCGCA TCAAGCAGAT CATCAACATG
1261 TGGCAGCGCG TGGGCCAGGC CATGTACGCC CCCCCATCG AGGGCAACAT CCGCTGCGAG
1321 AGCAACATCA CCGGCTGCT GCTGACCCGC GACGGCGGCA GCGGCGCAA CAGCAGCAAG
1381 GAGACCTACC GCCCCATCGG CGGCAACATG CGCGACAAC GGCAGCGA GCTGTACAAG
1441 TACAAGGTGG TGAAGATCGA GCCCATCGGC GTGGCCCCCA CCAAGGCCAA GCGCCGCGTG
1501 GTGGAGCGCG AGAAGCGCGC CATCGGCCCT GCGCGCGCT TCCTGGGCTT CCTGGGCGCC
1561 GCCGCGAGCA CCATGGGCGC CGCCAGCATG ACCCTGACCG TGCAGGCCCG CCAGCTGCTG
1621 AGCGGCATCG TGCAGCAGCA GAGCAACCTG CTGCGCGCCA TCGAGGCCCA GCAGCACCTG
1681 CTGAAGCTGA CCGTGTGGGG CATCAAGCAG CTGCAGGCC GCGTGCTGGC CGTGGAGCGC
1741 TACCTGAAGG ACCAGCAGCT GCTGGGCATC TGGGGCTGCA GCGGCAAGCT GATCTGCACC
1801 ACCAAGGTGC CCTGGAACAG CAGCTGGAGC AACAAGAGCC AGAGCGAGAT CTGGGGCAAC
1861 ATGACCTGGA TGCAGTGGGA CCGCGAGGTG ATCAACTACA CCAACATCAT CTACGACCTG
1921 ATCGAGGAGA GCCAGAACCA GCAGGAGAAG AACGAGCAGG ACCTGCTGGC CCTGGACAAG
1981 TGGGCCAGCC TGTGGAGCTG GTTCGACATC AGCAACTGGC TGTGGTACAT CAAGATCTTC
2041 ATCATCATCG TGGGCGGCCT GATCGGCCTG CGCATCGTGT TCGCCGTGCT GAGCATCATC
2101 AACCGCGCCG GCCAGGGCTA CAGCCCCCTG AGCCTGCAGA CCCTGACCCC CCACCCCGAG
2161 GGCCCCGACC GCCCCGCGCG CATCAAGGAG GAGGGCGGCG AGCAGGACCG CGACCCGAGC
2221 ATCCGCTGG TGAGCGGCTT CCTGGCCTG GCCTGGGACG ACCTGCGCAG CCTGTGCTG
2281 TTCAGTACC GCGCCTGCG CGACTTCATC AGCATCGCCG CCCGACCGT GGAGCTGCTG
2341 GGCCGCGACA GCCTGAAGGG CCTGCGCCTG GGCTGGGAGG GCCTGAAGTA CCTGGGCAAC
2401 CTGCTGGGCT ACCGCGGCCA GGAGCTGAAG AGCAGCGCCA TCAACCTGAT CGACACCATC
2461 GCCATCGCCG TGGCCGGCTG GACCGACCG GTGATCGAGA TCGGCCAGCG CTTCTGCCGC
2521 GCCATCCGCA ACATCCCCC CCGCATCCG CAGGGCGCG AGCGCGCCCT GCAGTAA

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FIGURE 12

gp160mod.SE8538

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1  ATGCGCGTGA AGGGCATCCA GCGCAACAGC CAGCACCTGC TGGCGTGGGG CACCATGATC
61 CTGGGCGATGA TCATCATCTG CAGCACC GCCAAGCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCGTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCTTAC
181 GACACCGAGG TGCACAACGT GTGGGCCACC CACGCCTGCG TGCCACCGA CCCCACCCC
241 CAGGAGCTGC ACCTGGCCAA CGTGACCGAG GAGTTCAACA TGTGGAAGAA CAGCATGGTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGATCCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGGAGTGC AACGACTACA ACTAACCGT GACCAACAGC
421 AGCCACAGCT ACAACGTGAC CAACATGCAG GAGATGAAGA ACTGCAGCTT CAACGTGACC
481 ACCGAGCTGC GCGACAAGCG CCAGAAGGTG ACCAGCCTGT TCTACAGCT GGACGTGGTG
541 CCCATCGGCG GCAACGACAC CAACAGCACC CAGTACCGCC TGATCAACTG CAACACCAGC
601 GCCATCACCC AGGCCGTGCC CAAGGTGACC TTCGAGCCCA TCCCCTCCA CTACTGCGCC
661 CCCGCCGGCT TCGCCATCCT GAAGTGCCGC GACGAGAACT TCAACGGCAC CGGCCCTTGC
721 AAGAACGTGA GCACCGTGCA GTGCACCCAC GGCATCAAGC CCGTGGTGAG CACCCAGCTG
781 CTGCTGAACG GCAAGCTGGC CCGCGAGAAG GTGATGATCC GCAGCGAGAA CATCAACCA
841 AACGTGAAGA ACATCATCTG GCAGCTGAAG GAGCCCGTGG AGATCAACTG CACCCGCCCC
901 GGCAACAACA CCCGCAAGAG CATCCGCATC GGCCCCGGCC AGGCCCTTCTA CGCCACCGGC
961 GAGGTGATCG GCGACATCCG CCAGGCCAC TGCAACGTGA GCCCGGCCAA GTGGAACAAG
1021 ACCCTGCACG AGGTGGCCAA GCAGCTGCCG ACCTACTTCA ACAACAAGAC CATCATCTTC
1081 ACCAACAGCA GCGGCGGCGA CCTGGAGATC ACCACCCACA CCGTGAAGTG CGGCGGCGAG
1141 TTCTTCTACT GCAACACCAG CGGCCTGTTC AACAGCACCT GGAGCAGCAA CGCCAGCGAG
1201 CCCATGAGCA ACAGCACCGA GAGCAACGAC ACCATCACCC TGCACTGCCG CATCCGCCAG
1261 ATCATCAACA TGTGGCAGCG CGCCGGCAAG GCCATCTACG CCCCCCATC CCCCCGCATC
1321 ATCAAGTGCG TGAGCAACAT CACCGGCTTG ATCCTGACCC GCGAAGGCGG CAGCAACAAC
1381 AGCACCAACG AGACCTTCCG CCCCAGCGGC GGCACATGC GCGACAAC TGCGCAGCGAG
1441 CTGTACAAGT ACAAGGTGGT GAAGATCGAG CCCCTGGGCG TGGCCCCAC CAAGGCCAAG
1501 CGCCGCGTGG TGGAGCGCGA GAAGCGCGCC ATCGGCATCG GCGCGTGTTC CATCGGCTTC
1561 CTGGGCGCGG CCGGCAGCAC CATGGGCGCC GCCAGCATCA CCCTGACCGT GCAGGCCCGC
1621 CAGCTGCTGA GCGGCATCGT GCAGCAGCAG AGCAACCTGC TGCGCGCCAT CGAGGCCAG
1681 CAGCACCTGC TGAAGCTGAC CGTGTGGGGC ATCAAGCAGC TGCAAGCCCG CGTGCTGGCC
1741 GTGGAGCGCT ACCTGAAGGA CCAGCAGCTG CTGGGCATCT GGGGCTGCAG CGGCAAGCTG
1801 ATCTGCACCA CCAACGTGCC CTGGAACAGC AGCTGGAGCA ACAAGAGCCA GAGCGAGATC
1861 TGGGACAACA TGACCTGGCT GCAGTGGGAC AAGGAGATCA GCAACTACAC CCAGACCATC
1921 TACCGCTGA TCGAGGAGAG CCAGAACCAG CAGGAGAAGA ACGAGCAGGA CCTGCTGGCC
1981 CTGGACAAGT GGGCCAGCCT GTGGAAGTGG TTCGACATCA GCCGCTGGCT GTGGTACATC
2041 CGCATCTTCA TCATGATCGT GGGCGGCTTG ATCGGCCTGC GCATCGTGTT CGCCGTGCTG
2101 AGCGTGATCA ACCGCGTGC CGAGGGCTAC AGCCCCCTGA GCTTCCAGAT CCACACCCCC
2161 AACCCTGGCG ACCTGGACCG CCCCAGCGGC ATCGAGGAGG AGGGCGGCGA GCAGGACCGC
2221 GGCCGCGAGC TCCGCTGGT GAGCGGCTTC CTGGCCCTGG CCTGGGACGA CCTGCGCAGC
2281 CTGTGCTGT TCAGCTACCA CCGCTGCGC GACTTCATCC TGATCGCCGC CCGCACCGTG
2341 GAGCTGCTGG GCCAGCGCGG CTGGGAGGGC CTGAAGTACC TGTGGAACCT GCTGGTGTAC
2401 TGGATCCGCG AGCTGAAGAT CAGCGCCATC AGCCTGCTGG ACACCATCGC CATCGCCGTG
2461 GCCGGCTGGA CCGACCGCGT GATCGAGCTG GGCCAGCGCC TGTGCCGCGC CATCCTGCAC
2521 ATCCCCGTGC GCATCCGCCA GGGCTTCGAG CGCGCCCTGC TGTA

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FIGURE 13

gp160mod.UG031

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1 ATGCGCGTGC GCGGCATCCA GACCAGCTGG CAGAACCTGT GGCCTGCGG CACCATGATC
61 CTGGGCATGC TGATGATCTA CAGCGCCGCC GAGAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCGTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCCTAC
181 GACACCGAGG TGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCCACGA CCCCACCCCC
241 CAGGAGATCC ACCTGGAGAA CGTGACCGAG GACTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGGAG
361 CTGACCCCCC TGTGCGTGAC CCTGGACTGC CTGAACGCCA CCCTGAACGC CACCGCCCCC
421 AACGTGACCA ACGACATGGA GGGCGAGATG AAGAACTGCA GCTACAACAT CACCACCGAG
481 CTGAAGGACA AGAAGCAGCA GGTGTACAGC CTGTTCTACA AGCTGGACGT GGTGCAGATC
541 AACGAGAAGA ACAAGACCAA CAAGTACCGC CTGATCAACT GCAACACCAG CGCCATCACC
601 CAGGCCTGCC CCAAGGTGAG CTTTCGAGCCC ATCCCCATCC ACTACTGCGC CCCC GCCGGC
661 TTCGCCATCC TGAAGTGCAA GGACACCGAG TTCAACGGCA CCGGCCCTGT CAAGAACGTG
721 AGCACCGTGC AGTGACCCCA CGGCATCCGC CCGTGATCA GCACCCAGCT GCTGCTGAAC
781 GGCAGCCTGG CCGAGGGCGG CATCCAGATC CGCAGCGAGA ACATCACCA CAACGCCAAG
841 ACCATCATCG TGCAGCTGGA CAAGGCCGTG AAGATCAACT GCACCCGCC CAACAACAAC
901 ACCCGCAAGA GCGTGCGCAT CGGCCCGGCG CAGGCCTTCT ACGCCACCGG CGACATCATC
961 GCGGACATCC GCCAGGCCCA CTGCAACGTG AGCCGCGCCA AGTGGAACTG GACCCCTGCGC
1021 GGCATCGCCA AGAAGCTGAG CGAGCACTTC AAGAACAAGA TCATCATCTT CGAGAAGAGC
1081 AGCGGGCGCG ACATCGAGAT CACCACCCAC AGCTTCAACT GCGGCGGCGA GTTCTTCTAC
1141 TGCAACACCA GCGGCCGTGT CAACGGCACC TGGAAGCCCA ACAGCACCAG GAGCAACAAC
1201 ACCAÇCCCA ACAGACCCAT CACCCTGACC TGCCGCATCA AGCAGATCAT CAACATGTGG
1261 CAGAAGGTGG GCCAGGCCAT GTACGCCCCC CCCATCCAGG GCGTGATCCG CTGCGAGAGC
1321 AACATACCG GCCTGCTGCT GACCCGCGAC GGCGGCATCA ACAGCATCAA CGAGACCTTC
1381 CGCCCCGCG GCGGCAACAT GCGCGACAAC TGGCGCAGCG AGCTGTACAA GTACAAGGTG
1441 GTGAAGATCG AGCCCTGGG CGTGGCCCCC AGCCGCGCCA AGCGCCGCGT GGTGGAGCGC
1501 GAGAAGCGCG CCGTGGGCAT CGGCGCCGTG TTCCTGGGCT TCCTGGGCGC CGCCGGCAGC
1561 ACCATGGGCG CCGCCAGCAT CACCCTGACC GCCCAGGCCG GCCAGCTGCT GAGCGGCATC
1621 GTGCAGCAGC AGAGCAACCT GCTGCGCGCC ATCAAGGCCG AGCAGCACAT GCTGAAGCTG
1681 ACCGTGTGGG GCATCAAGCA GTGCGAGGCC CGCGTGCTGG CCGTGGAGCG CTACCTGAAG
1741 GACCAGCAGC TGCTGGGCAT CTGGGGCTGC AGCGGCAAGC TGATCTGCAC CACCAACGTG
1801 CCCTGGAACA GCAGCTGGAG CAACAAGAGC ATGAACGAGA TCTGGGACAA CATGACCTGG
1861 CTGCAGTGGG AGAAGGAGAT CAGCAACTAC ACCCAGCTGA TCTACAACCT GATCGAGGAG
1921 AGCCAGAACC AGCAGGAGAA GAACGAGCAG GACCTGCTGG CCTGGACAA GTGGGCCAGC
1981 CTGTGGAAC TGTTCGACAT CAGCCGCTGG CTGTGGTACA TCAAGATCTT CATCATGATC
2041 GTGGGCGGCC TGATCGGCCT GCGCATCGTG TTCGCCGTGC TGAGCGTGAT CAAÇCGCGTG
2101 CGCCAGGGCT ACAGCCCCCT GAGCTTCCAG ATCCGCACCC CCAACCCCGA GGAGCCCGAC
2161 CGCCTGGGCC GCATCGGCCA GGAGGGCGGC GAGCAGGACC GCGACCGCAG CATCCGCTTG
2221 GTGAGCGGCT TCCTGGCCCT GGCCCTGGGAC GACCTGCGCA GCCTGTGCCT GTTCAGCTAC
2281 CACCGCCTGC GCGACTTCAT CAGCATCGCC GCCCGCACCG TGGAGCTGCT GGGCCACAGC
2341 AGCCTGAAGG GCCTGCGCCT GGGCTGGGAG GGCTGAAGT ACCTGTGGAA CCTGCTGCTG
2401 TACTGGGGCC TGGAGCTGAA GACCAGCGCC GTGAACCTGG TGGACACCAT CGCCATCGCC
2461 GTGGCCGGCT GGACCGACCG CGTGATCGAG ATCGGCCAGC GCATCTTCCG CGCCATCCTG
2521 AACATCCCCC GCCGCATCCG CCAGGGCCTG GAGCGCGGCC TGCTGTAA

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FIGURE 14

gp160mod.92UG001

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1  ATGCGCGTGC  GCGAGATCGA  GCGCAACTAC  CTGTGCCTGT  GCGGCTGGGG  CATCATGCTG
61  CTGGGCATGC  TGATGACCTA  CAGCGTGGCC  GAGAAGAAGT  GGGTGACCGT  GTACTACGGC
121  GTGCCCCTGT  GGAAGGAGGC  CACCACCACC  CTGTTCTGCG  CCAGCGACGC  CAAGAGCTAC
181  AAGACCGAGG  TGCACAACAT  CTGGGCCACC  CACGCCCTGCG  TGCCCAACCGA  CCCCACCCCC
241  CGCGAGATCG  AGCTGGAGAA  CGTGACCGAG  AACTTCAACA  TGTGGAAGAA  CAACATGGTG
301  GAGCAGATGC  ACGAGGACAT  CATCAGCCTG  TGGGACCAGA  GCCTGAAGCC  CTGCGTGAAG
361  CTGACCCCCC  TGTGCGTGAC  CCTGAAGTGC  ACCGACGCCC  GCCGCAACGA  GACCCGCAAC
421  AACATACCCG  GCATGGAGAA  CAACGACCAG  ATCGAGATGA  AGAAGTGCAG  CTTCACATC
481  ACCACCAAGC  TGATCGACAA  GAAGAAGCAG  GTGCACGCCC  TGTTCACCG  CCTGGACGTG
541  GTGCAGATCG  ACAACGACAC  CAGCAACAGC  AACTACAGCA  ACTACCGCCT  GATCAACTGC
601  AACACGACCG  CCATCACCCA  GGCCTGCCCC  AAGGTGACCT  TCGAGCCCAT  CCCCATCCAC
661  TACTGCGCCC  CCGCCGGCTT  CGCCATCCTG  AAGTGCCGCG  ACAAGAAGTT  CAACGGCACC
721  GGGCCCTGCA  AGAACGTGAG  CACCGTGACG  TGCACCCACG  GCATCCGCCC  CGTGGTGAGC
781  ACCCAGCTGC  TGCTGAACGG  CAGCCTGGCC  GAGGAGGAGA  TCATCATCCG  CAGCGAGAAC
841  CTGACCAACA  ACGCCAAGAC  CCTGATCGTG  CAGCTGAACG  AGAGCGTGGA  GATCAACTGC
901  ACCCGCCCCC  ACTACAACCA  GATCCGCCAG  CGCACCAGCA  TCGGCCAGGG  CCAGGCCCTG
961  TACACCACCC  GCGTGACCGG  CGACATCCGC  AAGGCCTACT  GCAACATCAG  CAAGGCCGGC
1021  TGGACAAGA  CCCTGCAGCA  GGTGGCCAAG  AAGCTGGGCG  ACCTGTTCAA  CCAGACCACC
1081  ATCATCTTCA  AGCCCAGCAG  CGGCGGCGAC  CCCGAGATCA  CCACCCACAG  CTTCACCTGC
1141  GGGCGCGAGT  TCTTCTACTG  CAACACCAGC  AAGCTGTTCA  ACAGCGCCTG  GAACGACAGC
1201  ACCTGGAACA  TCGGCAACAA  CAACACCGGC  AGCGACAACG  AGACCATCAT  CATCCCTGTC
1261  CGCATCAAGC  AGATCATCAA  CATGTGGCAG  GCGGTGGGCA  AGGCCATGTA  CGCCCCCCCC
1321  ATCGAGGGCT  GGATCAACTG  CGCCAGCAAC  ATCACCGGCC  TGCTGCTGGT  GCGCGACGGC
1381  GGGCGCGCCA  ACGACAGCCA  GAACGAGACC  TTCCGCCCCC  AGGGCGGCGA  CATGCGCGAC
1441  AACTGGCGCA  GCGAGCTGTA  CAAGTACAAG  GTGGTGAAGA  TCGAGCCCTT  GGGCATCGCC
1501  CCCACCAAGG  CCAAGCGCCG  CGTGGTGGAG  CGCGAGAAGC  GCGCCATCGG  CCTGGGCGCC
1561  ATGTTCTTGG  GCTTCCTGGG  CGCCGCCGGC  AGCACCATGG  GCGCCGCCAG  CCTGACCCCTG
1621  ACCGTGCAGG  CCCGCCAGCT  GCTGAGCGGC  ATCGTGACGC  ACCAGAACA  CCTGCTGATG
1681  GCCATCGAGG  CCCAGCAGCA  CCTGCTGCAG  CTGACCGTGT  GGGGCATCAA  GCAGCTGCAG
1741  GCGCGCATCC  TGGCCGTGGA  GCGCTACCTG  CAGGACCAGC  AGCTGCTGGG  CAGCTGGGGC
1801  TGCAGCGGCC  GCCACATCTG  CACCACCACC  GTGCCCTGGA  ACAGCAGCTG  GAGCAACAAG
1861  AGCATCGACG  ACATCTGGAA  CAACATGACC  TGGATGGAGT  GGGAGAAGGA  GATCGACAAC
1921  TACACCGGCG  TGATCTACCG  CCTGATCGAG  GAGAGCCAGA  CCCAGCAGGA  GAAGAACGAG
1981  CAGGAGCTGC  TGCAGCTGGA  CAAGTGGGCC  AGCCTGTGGA  ACTGGTTCAG  CATCACCAGG
2041  TGGCTGTGGT  ACATCAAGAT  CTTCATCATG  ATCGTGGGCG  GCCTGATCGG  CCTGCGCATC
2101  GTGTTACCCG  TGCTGAGCCT  GGTGAACCGC  GTGCGCCAGG  GCTACAGCCC  CCTGAGCTTC
2161  CAGACCTGT  TCCCCGCCCC  CGCGGGCCCC  GACCGCCCCG  AGGAGATCGA  GGAGGGCGGC
2221  GGCGAGCAGG  GCGCGGGCCG  CAGCACCCTG  CTGGTGAACG  GCTTCAGCAC  CCTGATCTGG
2281  GACGACCTGC  GCAACCTGTG  CCTGTTTACG  TACCACCGCC  TGCAGGACCT  GATCCTGATC
2341  GCCACCGGCA  TCGTGGAGCT  GCTGGGCCGC  CGCGGCTGGG  AGGCCATCAA  GTACCTGTGG
2401  AACCTGTGTC  AGTACTGGAG  CCAGGAGCTG  AAGACCAGCG  CCATCAGCCT  GTTCAACGCC
2461  ACCGCCGTGG  CCGTGGCCGA  GGGCACCAGC  CGCGTGATCG  AGGTGGTGCA  GCGCTTCTTC
2521  CGCGGCATCC  TGAACGTGCC  CACCCGCATC  CGCCAGGGCC  TGGAGCGCGC  CCTGCTGTAA

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FIGURE 15

gp160mod.94UG114

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1  ATGCGCGTGC GCGAGACCAA GCGCAACTAC CAGCACCTGT GGAAGTGGGG CACCATGCTG
61  CTGGGCATGC TGATGATCTG CAGCGTGACC GGCAAGAGCT GGGTGACCGT GTACTACGGC
121 GTGCCCCTGT GGAAGGAGGC CACCACCACC CTGTTCTQCG CCAGCGACGC CAAGGCCTAC
181 AAGGCCGAGG CCCACAACAT CTGGGCCACC CACGCCTGCG TGCCACCGA CCCCACCCC
241 CAGGAGATCA AGCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC ACCAACTGGG TGACCGACAC CACCAACACC
421 ACCGGCATGG CCAACTGCAG CTTCAACATC ACCACCGAGA TCCGCGACAA GAAGAAGCAG
481 GTGCAGGCCC GTTCTACAA GCTGGACGTG GTGAAGATCA ACGACAACGA CAGCGACAAC
541 ACCAGCTACC GCCTGATCAA CTGCAACACC AGCGCCATCA CCCAGGCTG CCCCAGATG
601 ACCTTCGAGC CCATCCCCAT CCACTACTGC GCCCCGCCG GCTTCGCCAT CCTGAAGTGC
661 AACGAGAAGA AGTTCAACGG CACCGGCCCC TGCAAGAACG TGAGCACCGT GCAGTGCACC
721 CACGGCATCA AGCCCGTGGT GAGCACCCAG CTGCTGCTGA ACGGCAGCCT GGCCGAGGAG
781 GAGATCATCA TCCGCGCGA GAACCTGACC AACAACGCCA AGATCATCAT CGGCTAGCTG
841 AACGAGAGCG TGCCCATCAA CTGCATCCGC CCCTACAACA ACACCCGCCA GAGCACCCGC
901 ATCGGCCCCG GCCAGGCCCT GTTCAACCACC AAGGTGATCG GCGACATCCG CCAGGCCAC
961 TGCAACATCA GCGGCGCCG CTGGAACAAG ACCCTGCAGC AGGTGGCCGA GAAGCTGGGC
1021 AACCTGCTGA ACCAGACCAC CATCATCTTC AAGCCAGCA GCGGCGCGA CCCCAGATC
1081 AACCCACA GCTTCAACTG CGGCGGCGAG TTCTTCTACT GCAACACCAC CCGCTGTTT
1141 AACAGCACCT GGAAGCGCAA CAACAGCGAG TGGCGCAGCG ACAACACCCC CGACGAGACC
1201 ATCACCTGC AGTGCCGCAT CAAGCAGATC ATCAACATGT GGCAGGAGGT GGGCAAGGCC
1261 ATGTACGCCC CCCCATCGA GGGCTTCATC AACTGCAGCA GCAACATCAC CGGCTGCTG
1321 CTGACCGCGC ACGGCGGCGC CATCAACAGC AGCCAGAACG AGACCTTCCG CCCCAGGCGC
1381 GCGGACATGC GCAACAACATG GCGCAGCGAG CTGTACAAGT ACAAGGTGGT GAAGCTGGAG
1441 CCCATCGGCC TGGCCCCCAC CGCCGCCAAG CGCCGCTGG TGGAGCGCGA GAAGCGCGCC
1501 ATCGGCCTGG GCGCCTGTT CTTGGGCTTC CTGGGCACCG CCGGCAGCAC CATGGGCGCC
1561 GTGAGCCTGA CCCTGACCGT GCAGGCCCGC CAGGTGCTGA GCGGCATCGT GCAGCAGCAG
1621 AACAACCTGC TGC GCGCCAT CGAGGCCAG CAGCACCTGC TGCAGCTGAC CGTGTGGGGC
1681 ATCAAGCAGC TGCAGGCCCG CATCCTGGCC GTGGAGAGCT ACCTGAAGGA CCAGCAGCTG
1741 CTGGGCATCT GGGGCTGCAG CGGCAAGCAC ATCTGCACCA CCAACGTGCC CTGGAACAGC
1801 AGCTGGAGCA ACCGCGAGCT GGACGAGATC TGGAACAACA TGACCTGGAT GGAGTGGGAG
1861 CGCGAGATCG ACAACTACAC CGAGCTGGTG TACAGCCTGC TGGAGGTGAG CCAGATCCAG
1921 CAGGAGAAGA ACGAGCAGGA GCTGCTGAAG CTGGACACCT GGGCCAGCCT GTGGAACCTG
1981 TTCAGCATCA CCCAGTGGCT GTGGTACATC AAGATCTTCA TCATGATCGT GGGCGGCTG
2041 ATCGGCCTGC GCATCGTGTT CGCCGTGCTG AGCGTGGTGA ACCGCGTGC CCAGGGCTAC
2101 AGCCCCCTGA GCTTCCAGAC CTGCTGCCC GCCCCCGCG AGCCGACCG CCCCAGGGC
2161 ATCGAGGAGG AGGGCGGCGA GCGCGACCGC GGCCGCAGCA TCCGCTGCT GAACGGCCTG
2221 AGCGCCCTGA TCTGGGACGA CTTGCGCAAC CTGTGCCTGT TCAGTACCA CCGCTGCGC
2281 GACCTGATCC TGATCGCCGC CCGCATCGTG GAGCTGCTGG GCCCGCGCG CTGGGAGGCC
2341 ATCAAGTACC TGTGGAACCT GCTGCAGTAC TGGATCCAGG AGCTGAAGAA CAGCGCCGTG
2401 AGCCTGTTCA ACACCATCGC CATCGCCGTG GCCGAGGGCA CCGACCGCG CATCGAGCTG
2461 GTGCAGCGCG CCGTGCGCGC CATCCTGAAC ATCCCCGTGC GCATCCGCCA GGGCTGGAG
2521 CGCGCCCTGC TGTA

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FIGURE 16

gp160mod.ELI

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1 ATGCGCGCCC GCGGCATCGA GCGCAACTGC CAGAACTGGT GGAAGTGGGG CATCATGCTG
61 CTGGGCATCC TGATGACCTG CAGCGCCGCC GACAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCTGT GGAAGGAGGC CACCACCACC CTGTTCTGCG CCAGCGACGC CAAGAGCTAC
181 GAGACCGAGG CCCACAACAT CTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCACCCCC
241 CAGGAGATCG CCCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC AGCGACGAGC TGCGCAACAA CGGCACCATG
421 GGCAACAACG TGACCACCGA GGAGAAGGGG ATGAAGAAGT GCAGCTTCAA CGTGACCACC
481 GTGCTGAAGG ACAAGAAGCA GCAGGTGTAC GCCCTGTTCT ACCGCTGGA CATCGTGCCC
541 ATCGACAACG ACAGCAGCAC CAACAGCACC AACTACCGCC TGATCAACTG CAACACCAGC
601 GCCATCACCC AGGCCTGCCC CAAGGTGAGC TTCGAGCCCA TCCCCATCCA CTACTGCGCC
661 CCCGCCGGCT TCGCCATCCT GAAGTGCCGC GACAAGAAGT TCAACGGCAC CGGCCCTGCG
721 ACCAACGTGA GCACCGTGCA GTGACCCACC GGCATCCGCC CCGTGGTGAG CACCCAGCTG
781 CTGCTGAACG GCAGCCTGGC CGAGGAGGAG GTGATCATCC GCAGCGAGAA CCTGACCAAC
841 AACGCCAAGA ACATCATCGC CCACCTGAAC GAGAGCGTGA AGATCACCTG CGCCCGCCCC
901 TACCAGAACA CCCGCCAGCG CACCCCCATC GGCCTGGGCC AGAGCCTGTA CACCACCCCG
961 AGCCGCAGCA TCATCGGCCA GGCCTACTGC AACATCAGCC GCGCCAGTG GAGCAAGACC
1021 CTGCAGCAGG TGGCCCGCAA GTGGGCACC CTGCTGAACA AGACCATCAT CAAGTTCAAG
1081 CCCAGCAGCG CGGCGGACCC CGAGATCACC ACCCAGAGCT TCAACTGCGG CGGCGAGTTC
1141 TTCTACTGCA ACACCAGCGG CCTGTCAAC AGCACCTGGA ACATCAGCGC CTGGAACAAC
1201 ATCACCGAGA GCAACAACAG CACCAACACC AACATCACCC TGCAGTGCCG CATCAAGCAG
1261 ATCATCAAGA TGGTGGCCGG CCGCAAGGCC ATCTACGCCC CCCCCATCGA CGGCAACATC
1321 CTGTGCAGCA GCAACATCAC CGGCCTGCTG CTGACCCGCG ACGGCGGCAT CAACAACAGC
1381 ACCAACGAGA CCTTCCGCCC CGGCGGCGGC GACATGCGCG ACAACTGGCG CAGCGAGCTG
1441 TACAAGTACA AGGTGGTGCA GATCGAGCCC CTGGGCGTGG CCCCCACCG CGCCAAGCGC
1501 CGCGTGGTGG AGCGCGAGAA GCGCGCCATC GGCCTGGGCG CCATGTTCTT GGGCTTCCTG
1561 GCGCGCGCCG GCAGCACCAT GGGCGCCCGC AGCGTGACCC TGACCGTGCA GGCCCGCCAG
1621 CTGATGAGCG GCATCGTGCA GCAGCAGAAC AACCTGCTGC GCGCCATCGA GGCCAGCAG
1681 CACCTGCTGC AGCTGACCGT GTGGGGCATC AAGCAGCTGC AGGCCCGCAT CCTGGCCGTG
1741 GAGCGCTACC TGAAGGACCA GCAGCTGCTG GGCATCTGGG GCTGCAGCGG CAAGCACATC
1801 TGCACCACCA ACGTGCCCTG GAACAGCAGC TGGAGCAACC GCAGCCTGAA CGAGATCTGG
1861 CAGAACATGA CCTGGATGGA GTGGGAGCGC GAGATCGACA ACTACACCGG CCTGATCTAC
1921 AGCCTGATCG AGGAGAGCCA GACCCAGCAG GAGAAGAACG AGAAGGAGCT GCTGGAGCTG
1981 GACAAGTGGG CCAGCCTGTG GAACTGGTTC AGCATCACCC AGTGGCTGTG GTACATCAAG
2041 ATCTTCATCA TGATCATCGG CGGCCTGATC GGCCTGCGCA TCGTGTTCGC CGTGCTGAGC
2101 CTGGTGAACC GCGTGCGCCA GGGCTACAGC CCCCTGAGCT TCCAGACCCT GCTGCCCCGC
2161 CCCC GCCGCC CCGACCGCCC CGAGGGCACC GAGGAGGAGG GCGGCGAGCG CGGCCGCGAC
2221 CGCAGCGTGC GCCTGTGTA GCGCTTCAGC GCCCTGATCT GGGACGACCT GCGCAGCCTG
2281 TGCCTGTTCA GCTACCACCG CCTGCGCGAC CTGATCCTGA TCGCCGTGCG CATCGTGGAG
2341 CTGCTGGGCC GCGCGGCTG GGCATCCTG AAGTACCTGT GGAACCTGCT GCAGTACTGG
2401 AGCCAGGAGC TGCGCAACAG CGCCAGCAGC CTGTTGACG CCATCGCCAT CGCCGTGGCC
2461 GAGGGCACCG ACCGCGTGAT CGAGATCATC CAGCGCGCCT GCGGCGCCGT GCTGAACATC
2521 CCCC GCCGCC TCCGCCAGGG CCTGGAGCGC AGCCTGCTGT AA

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FIGURE 17

gp160mod.93IN101

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1 ATGCGCGTGC GCGGCACCCT GCGCAACTAC CAGCAGTGGT GGATCTGGGG CGTGCTGGGC
61 TTCTGGATGC TGATGATCTG CAACGGCGGC GGCAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCTGT GGAAGGAGGC CAAGACCACC CTGCTGTGCG CCAGCGACGC CAAGGCCTAC
181 GAGCGCGAGG TGCACAACGT GTGGGCCACC CACGCTGCG TGCCACCGA CCCCAACCCC
241 CAGGAGATCG TGCTGGGCAA CGTGACCGAG AACTTCAACA TGTGGAGAA CGACATGGTG
301 GACCAGATGC ACGAGGACGT GATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGGAGTGC CGCAACGTGA GCCGCAACGT GAGCAGCTAC
421 AACACCTACA ACGGCAGCGT GGAGGAGATC AAGAACTGCA GCTTCAACGC CACCCCCGAG
481 GTGCGCGACC GCAAGCAGCG CATGTACGCC CTGTTCTACG GCCTGGACAT GTGCCCTTG
541 AACAAAGAAGA ACAGCAGCGA GAACAGCAGC GAGTACCGCC TGATCAACTG CAACACCAGC
601 GCCATCACCC AGGCCCTGCC CAAGGTGACC TTCGACCCCA TCCCCATCCA CTACTGCGCC
661 CCCGCCGGCT ACGCCATCCT GAAGTGCAAC AACAAAGACCT TCAACGGCAC CGGCCCTTGC
721 AACAACTGA GCACCGTGCA GTGCACCCAC GGCATCAAGC CCGTGGTGAG CAGCCCTGTG
781 CTGCTGAACG GCAGCCTGGC CGAGGGCGAG ATCATCATCC GCAGCGAGAA CCTGACCAAC
841 AACGTGAAGA CCATCATCGT GCACCTGAAC CAGAGCGTGG AGATCGTGTG CACCCGCCCC
901 AACAAACAACA CCCGCAAGAG CATCCGCATC GGGCCCCGCC AGACCTTCTA CGCCACCGGC
961 GACATCATCG GCGACATCCG CCAGGCCAC TGCAACATCA GCCGCGACAA GTGGAACGAG
1021 ACCCTGCAGC GCGTGGGCAA GAAGCTGGCC GAGCACTTCC ACAACAAGAC CATCAAGTTC
1081 GCCAGCAGCA GCGCGGCGGA CCTGGAGATC ACCACCCACA GCTTCAACTG CCGCGGCGAG
1141 TTCTTCTACT GCAACACCAG CGGCCTGTTT AACGGCACCT ACATGCCAC CTACATGCC
1201 AACGGCACCG AGAGCAACAG CAACAGCACC ATCACCATCC CCTGCCGAT CAAGCAGATC
1261 ATCAACATGT GGCAGGAGGT GGGCCGCGCC ATGTACGCCC CCCCATCGC CGGCAACATC
1321 ACCTGCACCA GCAACATCAC CGGCCTGCTG CTGGTGCACG ACGCGGGCAT CAAGGAGAAC
1381 GACACCGAGA ACAAGACCGA GATCTTCCG CCGGGCGCG GCGACATGCG CGACAATGG
1441 CGCAGCGAGC TGTACAAGTA CAAGGTGGTG GAGATCAAGC CCTGGGCGT GGGCCCCACC
1501 GCCGCCAAGC GCCGCGTGGT GGAGCGCGAG AAGCGCGCCG TGGGCATCGG CGCCGTGTTC
1561 CTGGGCTTCC TGGGCGCCGC CGGCAGCACC ATGGGCGCCG CCAGCATCAC CCTGACCGCC
1621 CAGGCCCCGC AGCTGCTGAG CGGCATCGTG CAGCAGCAGA GCAACCTGCT GCGCGCCATC
1681 GAGGCCACGC AGCACCTGCT GCAGCTGACC GTGTGGGGCA TCAAGCAGCT GCAGACCCGC
1741 GTGCTGGCCA TCGAGCGCTA CCTGAAGGAC CAGCAGCTGC TGGGCATCTG GGGCTGCAGC
1801 GGCAAGCTGA TCTGCACCAC CGCCGTGCCC TGGAACAGCA GCTGGAGCAA CAAGACCCAG
1861 AGCGAGATCT GGAACAACAT GACCTGGATG CAGTGGGACC GCGAGGTGAG CAACTACACC
1921 AACATCATCT ACAGCCTGCT GGAGGAGAGC CAGAACCAGC AGGAGAAGAA CGAGAAGGAC
1981 CTGCTGGCCC TGGACAGCTG GAAGAACCCTG TGGAGCTGGT TCGACATCAC CAACTGGCTG
2041 TGGTACATCA AGATCTTCAT CATGATCGTG GCGGCGCTGA TCGGCCTGCG CATCATCTTC
2101 GCCGTGCTGA GCATCGTGAA CCGCGTGC GC CAGGGCTACA GCCCCCTGAG CTTCCAGACC
2161 CTGACCCCCA ACCCCCGCGG CCCCAGCCGC CTGGGCGCA TCGAGGAGGA GGGCGCGAG
2221 CAGGACAAGG ACCGCAGCAT CCGCCTGGTG AACGGCTTCC TGGCCCTGGC CTGGGACGAC
2281 CTGCGCAACC TGTGCCTGTT CAGCTACCAC CGCCTGCGCG ACTTCATCAG CGTGGCCGCC
2341 CGCGTGGTGG AGCTGCTGGG CCGCAGCAGC TGGGAGGCC TGAAGTACCT GGGCAGCCTG
2401 GTGCAGTACT GGGGCTTGGG GCTGAAGAAG AGCGCCATCA GCCTGTTTGA CAGCATCGCC
2461 ATCGTGGTGG CCGAGGGCAC CGACCGCATC ATCGAGCTGG TGCAGGGCTT CTGCCGCGCC
2521 ATCCGCAACA TCCCCACCG CATCCGCCAG GGCTTCGAGG CCGCCCTGCA GTAA

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FIGURE 18
gp160mod.cm235.V3con

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1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
61 TCGCCCAGCG CTAGCAACAA CCTGTGGGTG ACCGTGTA CTGTTGGCGC
121 GACGCCGACA CCACCTGTGT CTGCGCCAGC GACGCCAAGG CCCACGAGAC CGAGGTGCAC
181 AACGTGTGGG CCACCCACGC CTGCGTGCCC ACCGACCCCA ACCCCCAGGA GATCCACCTG
241 GAGAACGTGA CCGAGAACTT CAACATGTGG AAGAACAACA TGGTGGAGCA GATGCAGGAG
301 GACGTGATCA GCCTGTGGGA CCAGAGCCTG AAGCCCTGCG TGAAGCTGAC CCCCCTGTGC
361 GTGACCCTGA ACTGCACCAA CGCCAAGCTG ACCAAGCTGA ACAACATCAC CAGCGTGAAC
421 AACACCATCG GCAACATCAC CGACGAGGTG CGCAACTGCA GCTTCAACAT GACCACCGAG
481 CTGCGCGACA AGAAGCAGAA GGTGCACGCC CTGTCTTACA AGCTGGACAT CGTGCCCATC
541 GAGGACAACA AGACCAGCAG CGAGTACCGC CTGATCAACT GCAACACCAG CGTGATCAAG
601 CAGGCCTGCC CCAAGATCAG CTTGACCCCC ATCCCCATCC ACTACTGCAC CCCC GCCGCG
661 TACGCCATCC TGAAGTGCAA CGACAAGAAC TTCAACGGCA CCGGCCCTCT CAAGAACGTG
721 AGCAGCGTGC AGTGACCCCA CGGCATCAAG CCCGTGGTGA GCACCCAGCT GCTGTGTAAC
781 GGCAGCCTGG CCGAGGAGGA GATCATCATC CGCAGCGAGA ACCTGACCAA CAACGCCAAG
841 ACCATCATCG TGCACCTGAA CAAGAGCGTG GAGATCAACT GCACCCGCC CAGCAACAAC
901 ACCCGCACCA GCATCACCAT CGGCCCGGCC CAGGTGTTCT ACCGCACCGG CGACATCATC
961 GGCACATCC GCAAGGCCTA CTGCGAGATC AACGGCACCA AGTGGAAACGA GGTGCTGACC
1021 CAGGTGACCG AGAAGCTGAA GGAGCACTTC AACAAACAAG CCATCATCTT CCAGCCCCC
1081 AGCGCGCGCG ACCTGGAGAT CACCATGCAC CACTTCAACT GCCGCGCGGA GTTCTTCTAC
1141 TGCAACACCA CCGCCTGTGT CAACAACACC TGATCGAGA ACGGCACCAT GGGCGGCTGC
1201 AACGGCACCA TCATCCTGCC CTGCAAGATC AAGCAGATCA TCAACATGTG GCAGGGCGCC
1261 GGCAGGCCA GTACGCCCC CCCCATCAGC GGCCGCATCA ACTGCGTGAG CAACATCACC
1321 GGCATCCTGC TGACCCGCGA CGGCGGCGCC ATCAACACCA CCAACGAGAC CTTCCGCCCC
1381 GGCAGCGGCA ACATCAAGGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCCACCCGC GCCAAGCGCC GCGTGGTGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CATGATCTTC GGCTTCTTGG GCGCCGCGG CAGCACCATG
1561 GGCAGCGGCA GCATCACCCT GACCGTGCAG GCGCGCCAGC TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GAAGGACCAG
1741 AAGTTCTTGG GCCTGTGGGG CTGCAGCGGC AAGATCATCT GCACCACCG CGTGCCCTGG
1801 AACAGCACCT GGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCCTGAC CGAGAGCCAG
1921 AACCAGCAGG ACCGCAACGA GAAGGACCTG CTGGAGCTGG ACAAGTGGGC CAGCCTGTGG
1981 AACTGGTTTG ACATCACCAG GTGGCTGTGG TACATCAAGA TCTTCATCAT GATCATCGGC
2041 GGCTGATCG GCCTGCGCAT CATCTTCGCC GTGCTGAGCA TCGTGAACCG CGTGCGCCAG
2101 GGCTACAGCC CCCTGAGCTT CCAGACCCCC TTCCACCACC AGCGCGAGCC CGACCGCAGC
2161 GAGCGCATCG AGGAGGGCGG CGCGGAGCAG GGCCGCGACC GCAGCGTGC CCGTGGTGAGC
2221 GGCTTCTTGG CCCTGGCCTG GGACGACCTG CGCAGCCTGT GCCTGTTTCA CTACCACCGC
2281 CTGCGCGACT TCATCCTGAT CGCCGCCCGC ACCGTGAAGC TGCTGGGCGG CAGCAGCCTG
2341 AAGGGCCTGC GCGCGGCTG GGAGGGCCTG AAGTACCTGG GCAACCTGCT GCTGTACTGG
2401 GGCCAGGAGC TGAAGATCAG CGCCATCAGC CTGCTGGAGC CCACCGCCAT CATCGTGGCC
2461 GGCTGGACCG ACCGCGTGAT CGAGGTGGCC CAGGGCGCCT GGCAGGCCAT CCGTGCACATC
2521 CCCCAGCGCA TCCGCCAGGG CCTGGAGCGC ACCCTGCTGT AA

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FIGURE 19

gp160partialmod.cm235.V3 con

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1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
61 TCGCCAGCG CTAGCAACAA CTTGTGGGTT ACAGTTTATT ATGGGGTTCC TGTGTGGAGA
121 GATGCAGATA CCACCCTATT TTGTGCATCA GATGCCAAAG CACATGAGAC AGAAGTGCAC
181 AATGTCTGGG CCACACATGC CTGTGTACCC ACAGACCCCA ACCCACAAGA AATACACCTG
241 GAAATGTAA CAGAAAATTT TAACATGTGG AAAAATAACA TGGTAGAGCA GATGCAGGAG
301 GATGTAATCA GTTTATGGGA TCAAAGTCTA AAGCCATGTG TAAAGTTAAC TCCTCTCTGC
361 GTTACTTTAA ATTGTACCAA TGCTAAGTTG ACCAATGTCA ATAACATAAC CAGTGTCTCT
421 AACACAATAG GAAATATAAC AGATGAAGTA AGAACTGTT CTTTTAATAT GACCACAGAA
481 CTAAGAGATA AGAAGCAGAA GGTCCATGCA CTTTTTTATA AGCTTGATAT AGTACCAATT
541 GAAGATAATA AGACTAGTAG TGAGTATAGG TTAATAAATT GTAATACTTC AGTCATTAAG
601 CAGGCTTGTC CAAAGATATC CTTTGATCCA ATTCCTATAC ATTATTGTAC TCCAGCTGGT
661 TATGCGATTT TAAAGTGTAA TGATAAGAAT TTCAATGGGA CAGGGCCATG TAAAAATGTC
721 AGTCAGTAC AATGCACACA TGGAAATTAAG CCAGTGGTAT CAACTCAATT GCTGTTAAT
781 GGCAGTCTAG CAGAAGAAGA GATAATAATC AGATCTGAAA ATCTCACAAA CAATGCCAAA
841 ACCATAATAG TGCACCTTAA TAAATCTGTA GAAATCAATT GTACCAGACC CTCCACAAT
901 ACAAGAACAA GTATAACTAT AGGACCAGGA CAAGTATTCT ATAGAACAGG AGACATAATA
961 GGAGATATAA GAAAAGCATA TTGTGAGATT AATGGAACAA AATGGRAATGA AGTTTAAACA
1021 CAGGTAAC TG AAAAATTTAA AGAGCACTTT AATAATAAGA CAATAATCTT TCAACCACCC
1081 TCAGGAGGAG ATCTAGAAAT TACAATGCAT CATTTTAATT GTAGAGGGGA ATTTTCTAT
1141 TGCAATACAA CACGACTGTT TAATAATACT TGCATAGAAA ATGGAACCAT GGGGGGGTGT
1201 AATGGCACTA TCATACTTCC ATGCAAGATA AAGCAAAATTA TAAACATGTG GCAGGGAGCA
1261 GGACAAGCAA TGTATGCTCC TCCCATCAGT GGAAGAATTA ATTGTGTATC AAATATTACA
1321 GGAATACTAT TGACAAGAGA TGGTGGTGCT ATTAATACAA CTAATGAGAC CTTCGCCCCC
1381 GCGCGCGGCA ACATCAAGGA CAAC TGCGCG AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCCACCCGC GCCAAGCGCC GCGTGGTGGG GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CATGATCTTC GGCTTCCTGG GCGCCGCCGG CAGCACCATG
1561 GCGCGCGCCA GCATCACCTT GACCGTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GAAGGACCAG
1741 AAGTTCCTGG GCCTGTGGGG CTGCAGCGGC AAGATCATCT GCACCACCGC CGTGCCCTGG
1801 AACAGCACCT GGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCCTGAC CGAGAGCCAG
1921 AACCAGCAGG ACCGCAACGA GAAGGACCTG CTGGAGCTGG ACAAGTGGGC CAGCCTGTGG
1981 AACTGGTTCG ACATACCAA GTGGCTGTGG TACATCAAAA TATTTATAAT GATAATAGGA
2041 GGTTTAATAG GTTTAAGGAT AATTTTGTCT GTGCTTTCTA TAGTGAATAG AGTTAGGCAG
2101 GGATACTCAC CTTTGTCTTT CCAGACCCCT TTCCATCATC AGAGGGAACC CGACAGATCC
2161 GAAAGAATCG AAGAAGGAGG TGGCGAGCAA GGCAGAGACA GATCCGTGCG ATTAGTGAGC
2221 GGATTCTTAG CTCTTGCGTG GGACGATCTA CGGAGCCTGT GCCTCTTCAG CTACCACCGC
2281 TTGAGAGACT TCATCTTGAT TGCAGCGAGG ACTGTGAAAC TTCTGGGACG CAGCAGTCTC
2341 AAGGGACTGA GACGGGGGTG GGAAGGTCTC AAATATCTGG GGAATCTTCT GTTATATTGG
2401 GGTCAAGAAC TAAAAATTAG CGCTATTTCT TTGCTTGATG CTACAGCAAT AATAGTAGCG
2461 GGGTGGACAG ATAGGGTTAT AGAAGTAGCA CAAGGAGCTT GGAGAGCCAT TCTCCACATA
2521 CCTAGGAGAA TCAGACAGGG CTTAGAAAGG ACTTTGCTAT AA

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FIGURE 20

Serum Binding Antibody Titers to HIV-1_{SF162} ENV Protein

Immunization	Replication-Competent Ad		Replication-Defective Ad	
	10 ⁷	10 ⁸	10 ⁸	10 ⁸
Post 1 st Ad	20	114.11	276.00	46.11
	20	390.91	N/A	72.06
	20	33.31		29.51
Post 2 nd Ad	2315.60	4242.53	114	55.57
	14380.44	8251.33	N/A	128.00
	372.87	2181.35		24.13
Post 1 st gp140	41175.45	43589.41	906	2675.15
	42411.99	51950.41	N/A	9448.33
	39974.95	36574.05		757.43
Post 2 nd gp140	19789.57	65799.55	14176	105578.03
	32906.06	68333.17	N/A	208905.20
	11901.37	63359.86		53357.79

FIGURE 21

Proliferative responses following Ad-HIVenv recombinant priming and
HIV_{SF162} oligomeric gp140 Δ V2 boosting

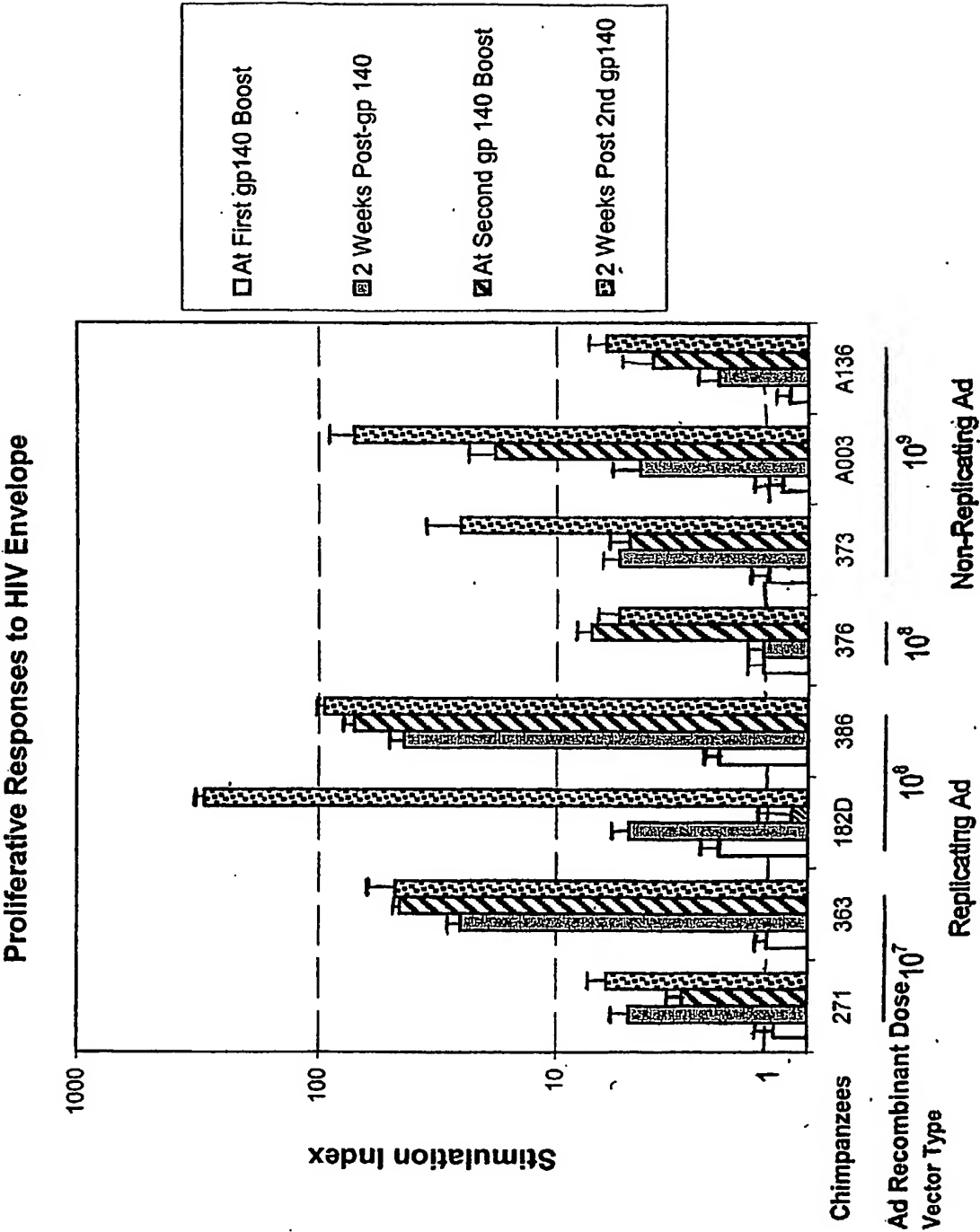
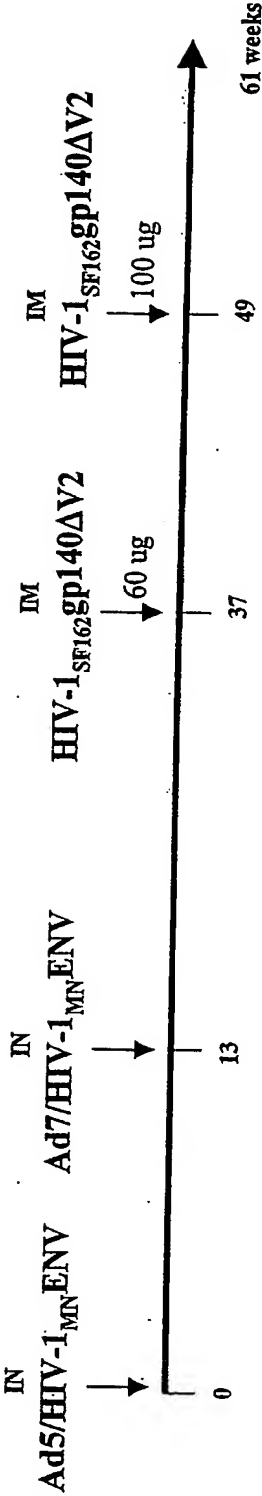


FIGURE 22

Immunization Regimen and Schedule



IN = intranasal; IM = intramuscular

Replication-competent Ad Vaccine Group		Replication-defective Ad Vaccine Group	
Chimpanzees	Priming Immunization (dose)	Chimpanzees	Priming Immunization (dose)
271, 363, A163	Ad5- or Ad7-ΔE3/HIV _{MN} Env (10 ⁷ pfu)	376, 360	Ad5- or Ad7-ΔE1E3/HIV _{MN} Env (10 ⁸ pfu)
182D, 386	Ad5- or Ad7-ΔE3/HIV _{MN} Env (10 ⁸ pfu)	373, A136, A003	Ad5- or Ad7-ΔE1E3/HIV _{MN} Env (10 ⁹ pfu)

Priming with replicating Ad-recombinant results in higher binding antibody titers

FIGURE 23A

Serum Binding Antibody Titers to HIV-1_{SF162} Env Protein

Animal Groups	Dose	2 nd Ad wk 15	1 st gp140 wk 39	2 nd gp140 wk 51
Replicating Ad	10 ⁷	475	3237	13462
Replicating Ad	10 ⁸	4242	43589	65799
Non-replicating Ad	10 ⁸	48	2784	21953
Non-replicating Ad	10 ⁹	56	2672	49005

** Higher titers to gp120 homologous to gp140 boost independent of vector (P = 0.0040)

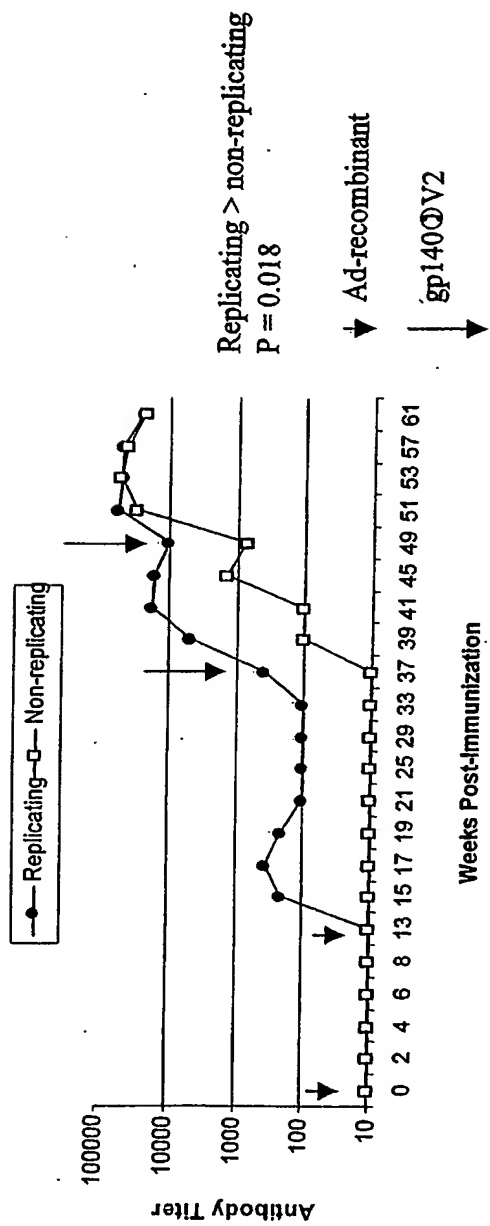
Serum Binding Antibody Titers to HIV-1_{IMB} Env Protein

Animal Groups	Dose	2 nd Ad wk 15	1 st gp140 wk 39	2 nd gp140 wk 51
Replicating Ad	10 ⁷	397	3794	28360
Replicating Ad	10 ⁸	68	4021	213307
Non-replicating Ad	10 ⁸	10	51	10471
Non-replicating Ad	10 ⁹	22	161	49570

* Higher titers to gp120 heterologous to gp140 boost in groups primed with replicating Ad-recombinants (P = 0.018).

Kinetics of Serum Binding Antibody Titers to HIV-1_{IMB} Env Protein

FIGURE 23B



Induction of Cross-Clade Binding Antibodies

FIGURE 24A

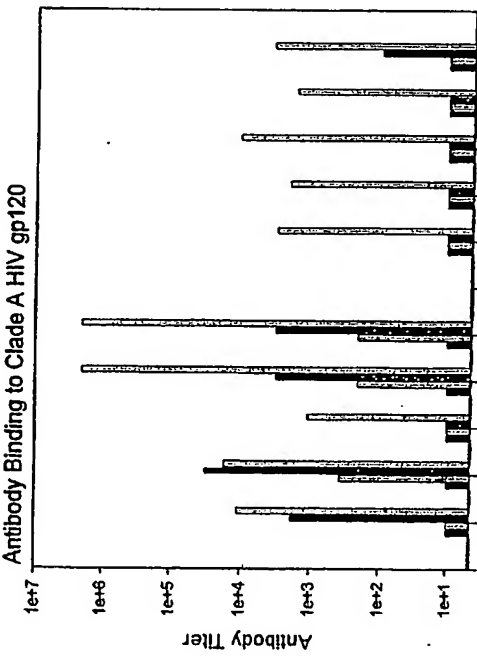


FIGURE 24C

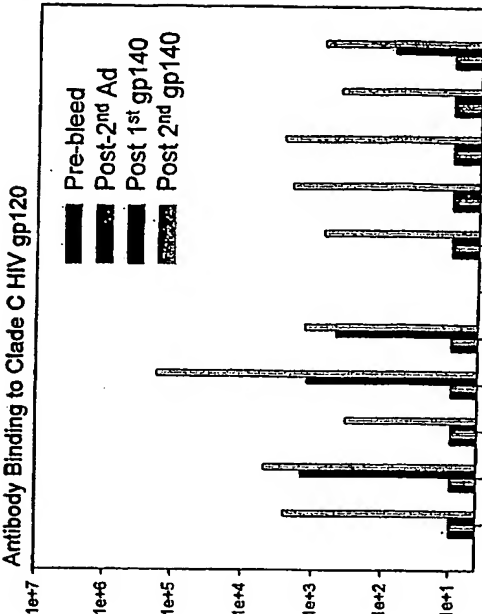


FIGURE 24B

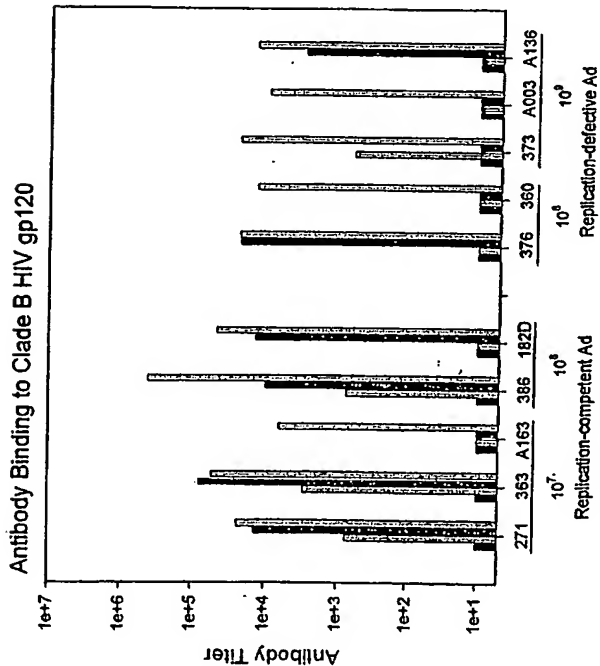
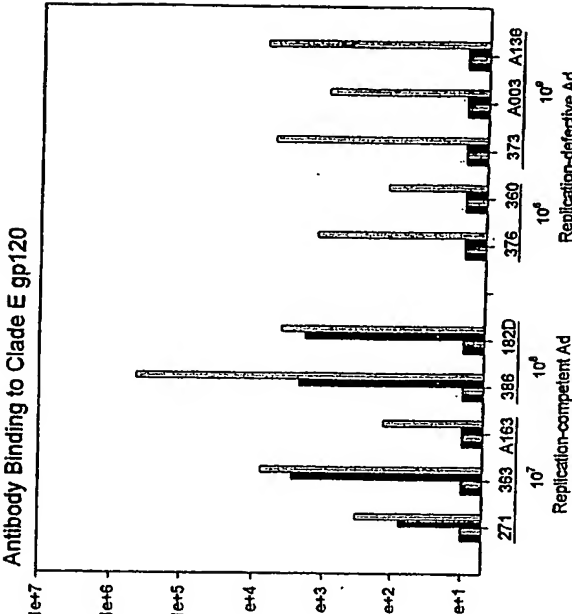


FIGURE 24D



**Replicating Ad-HIV recombinants are more effective
at priming neutralizing antibody responses**

FIGURE 25A

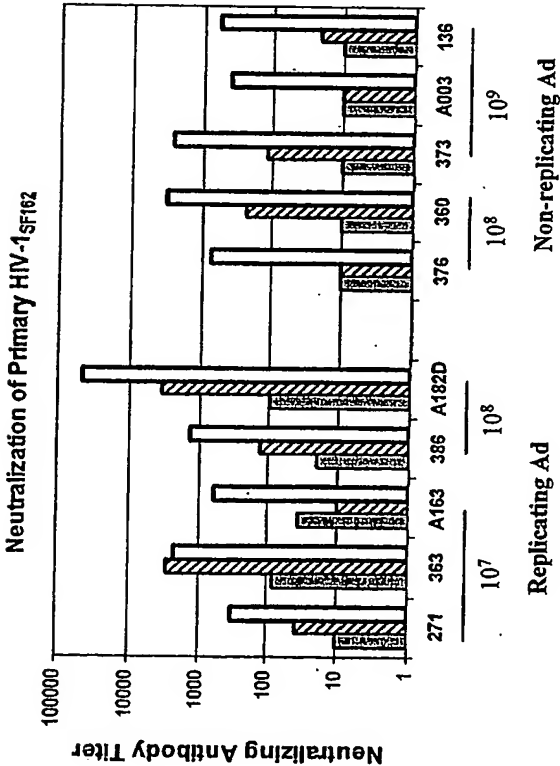
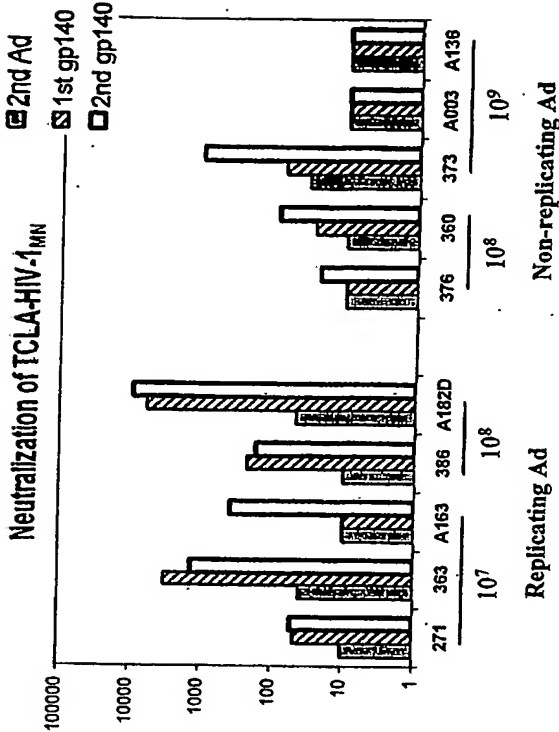


FIGURE 25B



Replicating > non-replicating; p = 0.012

FIGURE 26

Induction of neutralizing antibodies to clade C HIV_{TV-1} following a clade B immunization regimen.

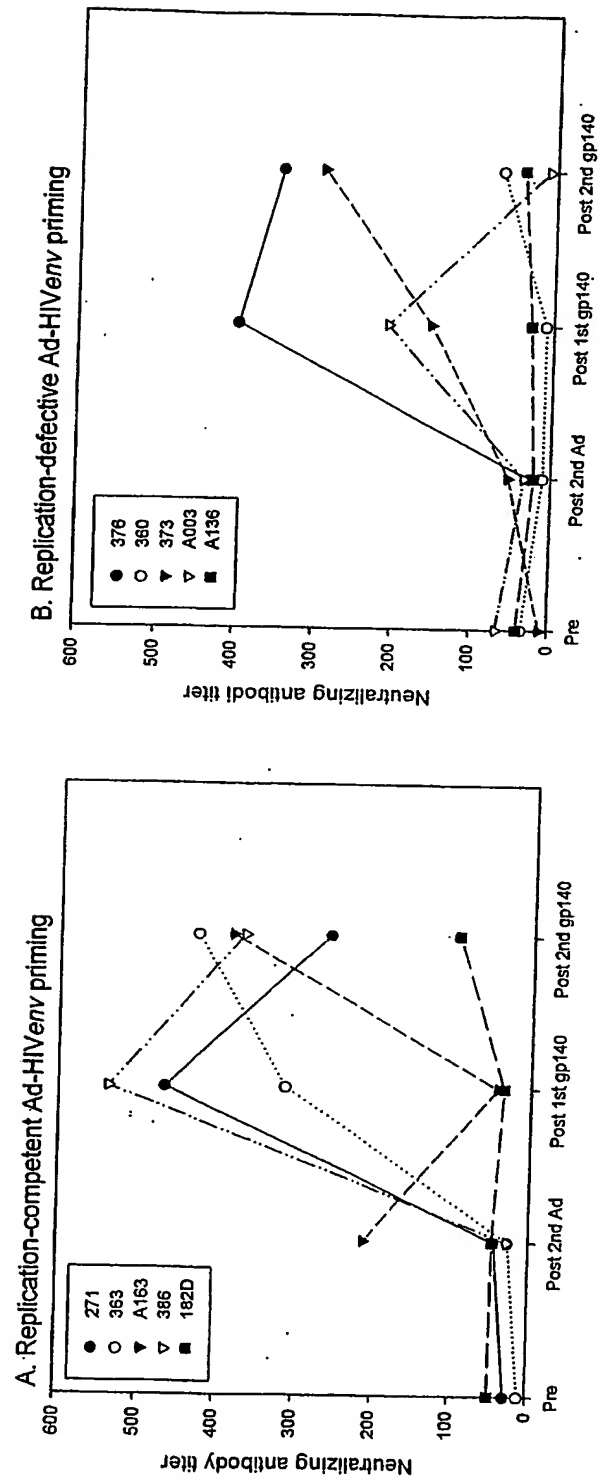
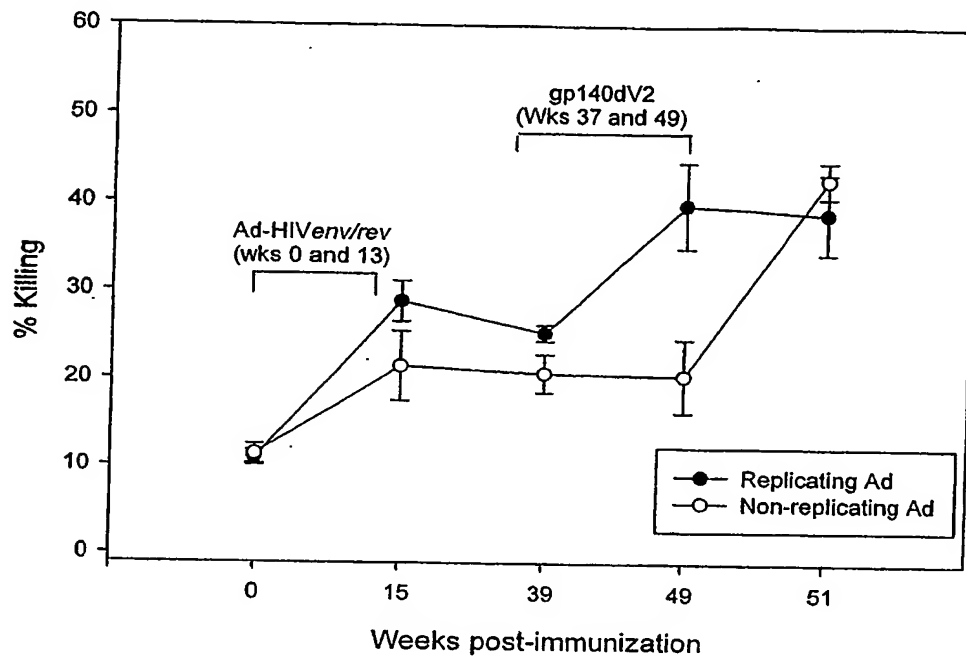


FIGURE 27

Induction of antibody-dependent cellular cytotoxicity (ADCC) activity by an Ad-HIV_{MN}env/rev priming/oligomeric gp140dV2 boosting regimen

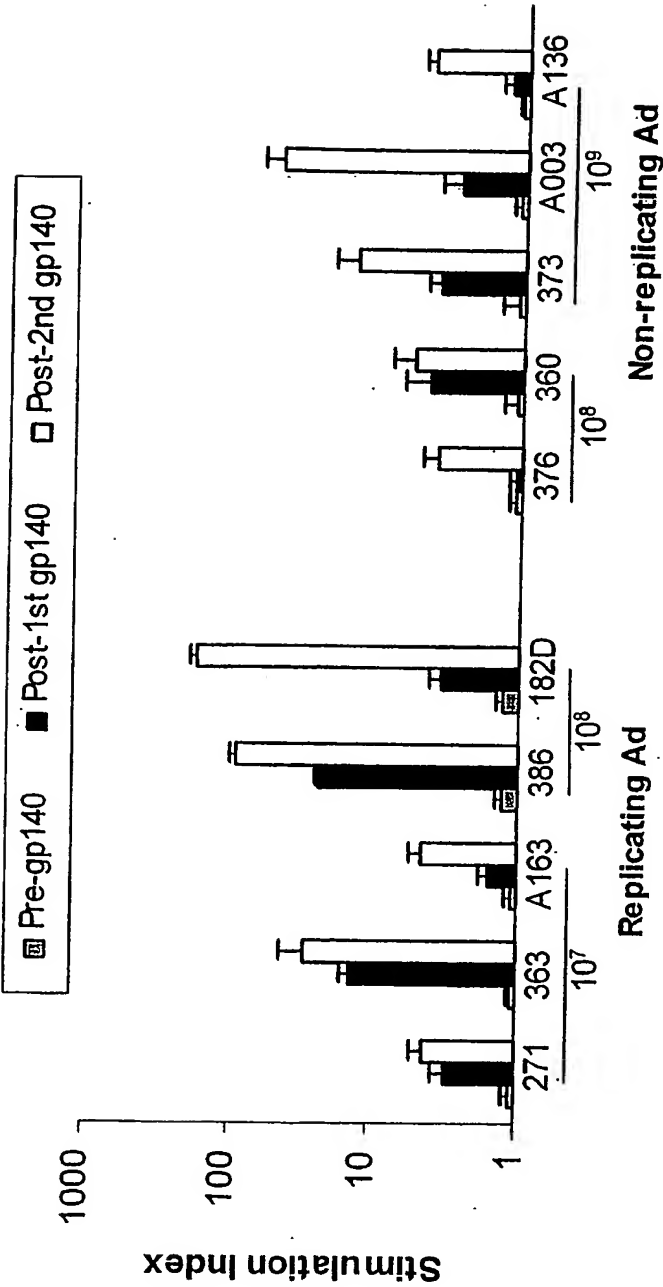


Chimpanzees were immunized intranasally with Ad5-HIV_{MN}env/rev (wk 0) and with Ad7-HIV_{MN}env/rev (wk 13). They were boosted with oligomeric HIV_{SF162} gp140 dV2 in MF-59 adjuvant at weeks 37 and 49. ADCC activity was determined using human PBMC as effectors and HIV_{IIIB} gp120-coated CEM-NK^r cells at an E:T of 50:1. Ten-fold serum dilutions were evaluated. Positive killing was defined as % killing by the negative control + 3 S.D. (20.4%).

A significant increase in % killing over weeks 15 to 51 was seen in chimpanzees primed with the replication-competent Ad-recombinants compared to the replication-defective Ad-recombinants ($P = 0.022$).

FIGURE 28

Replicating Ad-HIV recombinants are better at priming T-cell proliferative responses than non-replicating Ad-HIV recombinants



Post-2nd gp140: Replicating > Non-replicating, $p = 0.022$
Over all 3 time points, there is a linear trend of replicating > non-replicating, $p = 0.010$

FIGURE 29

Replicating Ad /HIV_{MN}^{env/rev} Induces More IFN- γ Secreting Cells at the Same or Lower Dose Compared to Non-replicating Ad /HIV_{MN}^{env/rev}

